

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:43:13 ; Search time 86 Seconds
(without alignments)
365.440 Million cell updates/sec

Title: US-09-995-593a-5

Perfect score: 1116

Sequence: 1 SGQFELILSMQNVNGELQN.....YACDQNGKTCMEGWGMEPC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1010	20 AAW87896	Human JAGGED1 solu
2	1116	100.0	1036	18 AAW18351	Proliferation and
3	1116	100.0	1187	18 AAW18352	Proliferation and
4	1116	100.0	1208	19 AAW40827	Human Jagged prote
5	1116	100.0	1218	19 AAW44301	Human serrate 1.
6	1116	100.0	1218	20 AAW87894	Human JAGGED1 prot
7	1116	100.0	1218	23 ABB07822	Human notch agonis
8	1116	100.0	1218	24 ABB97800	Amino acid sequenc
9	1116	100.0	1218	24 ABB72569	Human Notch ligand

10	1116	100.0	1218	24 AAE34031	Human notch ligand
11	1116	100.0	1218	24 ABB55874	Human notch ligand
12	1109	99.4	296	24 ABB97797	Amino acid sequenc
13	1109	99.4	1218	17 AAW05833	Human Serrate-1 (H
14	1109	99.4	1218	21 AAY59597	Human Serrate prot
15	1109	99.4	1218	23 AAW84344	Protein JAG1 diffe
16	1102	99.3	1218	18 AAW18354	Proliferation and
17	1102	98.7	1218	24 AAE34030	Murine notch ligand
18	1102	98.7	1218	24 ABB55876	Mouse notch ligand
19	1073	96.1	192	18 AAW18350	Proliferation and
20	970	86.9	1193	17 AAW05835	Chick Serrate. Ga
21	970	86.9	1193	21 AAY59599	Human Serrate prot
22	652	58.4	214	19 AAW44297	Human serrate 2 pr
23	652	58.4	1055	19 AAW44298	Human serrate 2 pr
24	652	58.4	1212	19 AAW44299	Human serrate 2.
25	652	58.4	1237	24 ABB55875	Human notch ligand
26	652	58.4	1238	23 ABB07823	Amino acid sequenc
27	652	58.4	1238	24 ABB97801	Human Notch ligand
28	652	58.4	1238	24 ABB72570	Human notch ligand
29	637	57.1	1237	24 AAE34032	Human notch ligand
30	584.5	52.4	1148	20 AAW87895	Human JAGGED2 prot
31	447	40.1	1404	14 AAR38304	Sequence of a serr
32	446	40.0	293	15 AAO27057	Serrate protein se
33	446	40.0	1404	21 AAY59600	Drosophila Serrate
34	446	40.0	1404	22 ABB61998	Drosophila melanog
35	446	40.0	1404	23 ABB07827	Drosophila notch a
36	433.5	38.8	727	18 AAW11719	C-Delta-1 polypept
37	433.5	38.8	740	18 AAW00876	Proliferation and
38	431	38.6	200	18 AAW18347	Truncated human de
39	431	38.6	200	20 AAW75493	Truncated human de
40	431	38.6	512	20 AAW75494	Truncated human de
41	431	38.6	520	18 AAW18348	Proliferation and
42	431	38.6	702	18 AAW18349	Proliferation and
43	431	38.6	702	20 AAW75495	Truncated human de
44	431	38.6	723	18 AAW18353	Proliferation and
45	431	38.6	723	20 AAW94498	Human delta-1 prot

ALIGNMENTS

RESULT 1
AAW87896
ID AAW87896 standard; Peptide; 1010 AA.
XX
AC AAW87896;
XX
DT 26-APR-1999 (first entry)
XX
DE Human JAGGED1 soluble polypeptide.
XX
JAGGED; JAGGED1; hJAGGED1; human; notch ligand; stem cell;
progenitor cell; haematopoiesis; cell differentiation;
KX Alagille syndrome; Leukaemia; lymphoma; diagnosis; therapy.
KW
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT Domain 22..1010
FT Region /note= "mature protein"
FT Region 185..239
FT Region /note= "Delta/Serrate/Lag-2 (DSL) domain"
FT Region 234..862
FT Region /note= "EGF-like repeat region"
XX WO9858958-A2.
XX
PD 30-DEC-1998.
XX
PF 25-JUN-1998; 98WO-US13207.
XX

PR 25-JUN-1997; 97US-0882046.
XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA (UNIW) UNIV WASHINGTON.
XX Hood L, Krantz ID, Li L, Spinner NB;
XX WPI; 1999-081220/07.
XX New Jagged peptides for inhibiting differentiation of progenitor
PT cells - also used for maintaining these cells in undifferentiated
PT state, e.g. for haematopoietic reconstitution
XX Claim 8; Page -: 101pp; English.
XX This is the amino acid sequence of a biologically active soluble
CC human JAGGED1 (hJAGGED) polypeptide comprising amino acid residues
CC 1-1010 of hJAGGED1 (see AAW87894). It was prepared by PCR
CC amplification (see AAV63759-60) of hJAGGED1 cDNA (see AAV63753) and
CC expression in CHO and BHK cells. hJAGGED1 is an activating ligand
CC for Notch protein that is expressed in bone marrow stromal cells.
CC A stromal cell line expressing hJAGGED1 permits survival and
CC proliferation of haematopoietic progenitor cells expressing Notch
CC but inhibits granulocyte differentiation. hJAGGED1 and active
CC peptides can be used (i) to inhibit differentiation of haematopoietic
CC progenitor cells (HPC), e.g. for subsequent production of blood cells
CC for transplantation or dendritic cells for immunotherapy, and (ii) to
CC maintain HPC in the undifferentiated state, particularly totipotent
CC cells or cells able to reconstitute the haematopoietic system, e.g.
CC in patients with leukaemia or lymphoma. Treated HPC, e.g. where
CC taken from a neonate, may be cryopreserved for many years, then
CC thawed for further expansion and differentiation. Optionally
CC JAGGED polypeptides are provided by transformed host cells.
CC (N.B. the amino acid sequence of the polypeptide of AAW87896 was
CC constructed from the full-length hJAGGED1 amino acid sequence given
CC in Fig1B of the specification).

XX SQ Sequence 1010 AA;
Query Match 100.0%; Score 1116; DB 20; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQFELEILSMQNVNGLQNGCCGARNPGRKCTRDECDTYFKVCLKEYQSRVTAGP 60
DB 32 SQFELEILSMQNVNGLQNGCCGARNPGRKCTRDECDTYFKVCLKEYQSRVTAGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 120
DB 92 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 151
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 211
QY 181 CDQNGNKTCEGMGMGPEC 198
DB 212 CDQNGNKTCEGMGMGPEC 229

RESULT 2
AAW18351
ID AAW18351 standard; protein; 1036 AA.
XX AC AAW18351;
XX DT 11-FEB-1998 (first entry)
XX Proliferation and differentiation suppression polypeptide.
DE DE
XX Proliferation; differentiation; suppression; human; delta-1;
KW serrate-1; blood cell; neuron; leukaemia; malignant tumour;
KW immunosuppression.

XX OS Homo sapiens.
XX PN WO9719172-A1.
XX 29-MAY-1997.
XX 15-NOV-1996; 96WO-JP03356.
XX 30-NOV-1995; 95JP-0311811.
PR 17-NOV-1995; 95JP-0299611.
XX (ASAH) ASAH KASEI KOGYO KK.
XX Itoh A, Sakano S;
XX WPI; 1997-298110/27.
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
PT proliferation and differentiation of undifferentiated human blood
PT cells
XX Claim 5; Page 66-71; 114pp; Japanese.
XX The present sequence represents a polypeptide which suppresses
CC proliferation and differentiation of undifferentiated cells such
CC as neurons and blood cells. The polypeptide may be used for the
CC prevention and control of disorders involving undifferentiated
CC cells, such as leukaemia and malignant tumours, and improvement of
CC blood formation, e.g. after immunosuppression.
XX SQ Sequence 1036 AA;
Query Match 100.0%; Score 1116; DB 18; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQFELEILSMQNVNGLQNGCCGARNPGRKCTRDECDTYFKVCLKEYQSRVTAGP 60
DB 1 SQFELEILSMQNVNGLQNGCCGARNPGRKCTRDECDTYFKVCLKEYQSRVTAGP 60
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 120
DB 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 120
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 180
DB 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 180
QY 181 CDQNGNKTCEGMGMGPEC 198
DB 181 CDQNGNKTCEGMGMGPEC 198

RESULT 3
AAW18352
ID AAW18352 standard; protein; 1187 AA.
XX AC AAW18352;
XX DT 11-FEB-1998 (first entry)
XX Proliferation and differentiation suppression polypeptide.
DE DE
XX Proliferation; differentiation; suppression; human; delta-1;
KW serrate-1; blood cell; neuron; leukaemia; malignant tumour;
KW immunosuppression.
XX OS Homo sapiens.
XX PN WO9719172-A1.
XX 29-MAY-1997.
PD

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XX 15-NOV-1996; 96WO-JP03356.
XX
PF 30-NOV-1995; 95JP-0311811.
PR 17-NOV-1995; 95JP-0299611.
XX
PA (ASAH ) ASAH KASEI KOGYO KK.
XX
PI Itoh A, Sakano S;
XX
DR WPI; 1997-298110/27.
XX
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
PT proliferation and differentiation of undifferentiated human blood
PT cells
XX
XX Claim 6; Page 71-76; 114pp; Japanese.
XX
XX The present sequence represents a polypeptide which suppresses
CC proliferation and differentiation of undifferentiated cells such
CC as neurons and blood cells. The polypeptide may be used for the
CC prevention and control of disorders involving undifferentiated
CC cells, such as leukaemia and malignant tumours, and improvement of
CC blood formation, e.g. after immunosuppression.
XX
SQ Sequence 1187 AA;

Query Match 100.0%; Score 1116; DB 18; Length 1187;
Best Local Similarity 100.0%; Pred. No. 1.2e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQQFELELLSMQNVNGELQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 1 SQQFELELLSMQNVNGELQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 60
Oy 61 CSFGSGSTPVIIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPSI 120
Db 61 CSFGSGSTPVIIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPSI 120
Oy 121 IEKASHGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 121 IEKASHGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Oy 181 CDQNGNKTCEGWMGPEC 198
Db 181 CDQNGNKTCEGWMGPEC 198

RESULT 4
AAW40827
ID AAW40827 standard; Protein; 1208 AA.
XX
AC AAW40827;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human Jagged protein.
XX
KW Jagged; Notch; angiogenesis; endothelial cell; migration; human;
KW wound repair; vulnery; injury repair; signal transduction;
KW motor neurone disease; amyotrophic lateral sclerosis; polymyeltis;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..11
FT Domain 175..220
FT /note= "DSL (Delta, Serrate, Lag-2 and Apx-1)
FT domain"
FT Region 224..852
FT /note= "EGF-like repeat region-containing 16

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FT Misc-difference 526 EGF repeats"
FT /note= "encoded by ANC"
FT Region 853..992
FT /note= "cysteine-rich region"
FT Domain 1058..1083
FT /note= "transmembrane domain"
FT Region 1084..1208
FT /note= "cytoplasmic region"
FT
PN W09745143-AL.
XX
XX 04-DEC-1997.
PD
XX 30-MAY-1997; 97WO-US09407.
PF
XX 31-MAY-1996; 96US-0018841.
PR
XX (NAAM-) NAT AMERICAN RED CROSS.
PA (UYGE-) UNIV GENEVE.
PA
XX
PI Maciag T, Montesano R, Pepper M, Wong MK, Zimrin AB;
XX
DR WPI; 1998-032340/03.
DR N-PSDB; AAV03674.
XX
XX New human Jagged protein - used to inhibit or promote angiogenesis
PT and to control migration of endothelial cells in injured blood
PT vessels
XX
PS Claim 2; Page 54-61; 81pp; English.
XX
XX This sequence comprises the human homologue of the rat Jagged
CC protein. Jagged is able to bind Notch protein and is involved in
CC endothelial cell (EC) migration and differentiation. The human
CC Jagged amino acid sequence was deduced from a human endothelial
CC cell cDNA (see AAV03674) induced by exposure to fibrin. Jagged
CC polypeptides can be expressed in host cell systems. A method for
CC treating or preventing disease by administering an agent that
CC (ant)agonises, inhibits, prevents, enhances or stimulates function
CC of the Notch or Jagged proteins is claimed, as well as a method for
CC affecting differentiation of mesoderm, endoderm, ectoderm and/or
CC neuroderm cells. When Jagged is applied to a micro-diameter blood
CC vessel from which ECs have been removed, damaged or reduced, it
CC decrease migrations of EC to the site, but when delivered to a
CC similar site on a large vessel it increases EC migration. Jagged
CC and its agonists are used to inhibit or prevent angiogenesis (where
CC associated with solid tumours, rheumatoid arthritis, inflammation,
CC or restenosis, particularly preventing angiogenesis from the vaso-
CC vasorum and promoting large vessel EC migration to repair the lumen
CC of large vessels). Anti-Jagged and Jagged antagonists (e.g.
CC antisense Jagged and Jagged mutants) are used to promote or enhance
CC angiogenesis, particularly for wound and injury repair, e.g. where
CC surgical, traumatic and/or caused by disease, e.g. diabetes-related
CC (all claimed). Angiogenesis can be modulated in vitro or in vivo
CC and expression of proteins by gene therapy is included. Modulation
CC of the Notch-Jagged signalling pathway may also be involved in
CC placental development and motor neurone diseases such as
CC amyotrophic lateral sclerosis, poliomyelitis etc.
XX
SQ Sequence 1208 AA;

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Query Match 100.0%; Score 1116; DB 19; Length 1208;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 SQQFELELLSMQNVNGELQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 81
Oy 61 CSFGSGSTPVIIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPSI 120
Db 82 CSFGSGSTPVIIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPSI 141

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QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 142 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 201
QY 181 CDQNGNKTCEGWMGPEC 198
DB 202 CDQNGNKTCEGWMGPEC 219

RESULT 5
AAW44301
ID AAW44301 standard; Protein; 1218 AA.
XX AAW44301;
XX 19-JUN-1998 (first entry)
XX Human serrate 1.
XX Human; serrate 2; regulation; stem cell; differentiation; neoplasm;
KW leukaemia; endothelial cell; tumour.
XX Homo sapiens.
XX Key
FH Peptide 1..31 Location/Qualifiers
FT Protein /label= Signal
FT Protein 32..1218
FT Protein /label= Serrate-1
XX WO9802458-A1.
XX 22-JAN-1998.
XX 11-JUL-1997; 97WO-JP02414.
XX 14-MAY-1997; 97JP-0124063.
XX 16-JUL-1996; 96JP-0186220.
XX (ASAH ) ASahi KASEI KOGYO KK.
XX Itoh A, Sakano S;
XX WPI; 1998-110528/10.
XX N-PSDB; AAV15201.
XX Human serrate-2 gene expression products - used to regulate stem
PT cell differentiation, useful in treating neoplasms, e.g. leukaemia
XX Disclosure; Page 77-86; 103pp; Japanese.
XX The present sequence represents human serrate 1, from the present
CC invention which describes human serrate 2, the present invention also
CC describes a method for the preparation of the polypeptides, and
CC antibodies binding to the polypeptide and its fragments. The polypeptide
CC and its fragments expressed by the serrate-2 gene can be used to inhibit
CC stem (especially blood stem) cell differentiation and to inhibit
CC endothelial cell growth. They may be incorporated in a cell culture
CC media for culturing undifferentiated stem cells. They can also be used
CC for treatment of neoplasms such as leukaemia. The antibodies can be used
CC for the diagnosis of malignant tumours.
XX Sequence 1218 AA:

Query Match 100.0%; Score 1116; DB 19; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQFEILEILSMQNVGELQNGCCGARNPGDKCTRQPCDYYFKVCLKEYOSRVTAGP 60
DB 32 SQFEILEILSMQNVGELQNGCCGARNPGDKCTRQPCDYYFKVCLKEYOSRVTAGP 91

QY 61 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPESFAWPSRYTLLVEAWSSNDTVQPDSI 120
DB 92 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPESFAWPSRYTLLVEAWSSNDTVQPDSI 151
QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 6
AAW87894
ID AAW87894 standard; Protein; 1218 AA.
XX AAW87894;
XX 26-APR-1999 (first entry)
XX Human JAGGED1 protein.
XX JAGGED; JAGGED1; human; notch ligand; stem cell;
KW progenitor cell; haematopoiesis; cell differentiation;
KW Alagille syndrome; leukaemia; lymphoma; diagnosis; therapy.
XX Homo sapiens.
XX Key
FH Peptide 1..21 Location/Qualifiers
FT Protein /note= "signal peptide"
FT Protein 22..1218 /note= "mature protein"
FT Domain 185..239
FT Region 234..862 /note= "Delta/Serrate/Lag-2 (DSL) domain"
FT Region 863..1012 /note= "EGF-like repeat region"
FT Domain 1077..1091 /note= "cysteine-rich region"
FT Peptide 188..204 /note= "transmembrane domain"
FT Peptide 178..240 /note= "this peptide is specifically claimed in Claim 1"
FT Protein 1..1010 /note= "this soluble peptide is specifically claimed in Claim 8"
FT Protein 1..1010 /note= "this soluble protein is specifically claimed in Claim 8"
XX WO9858958-A2.
XX 30-DEC-1998.
XX 25-JUN-1998; 98WO-US13207.
XX 25-JUN-1997; 97US-0882046.
XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX (UNIW ) UNIV WASHINGTON.
XX Hood L, Krantz ID, Li L, Spinner NB;
XX WPI; 1999-081220/07.
XX N-PSDB; AAV63753.
XX New Jagged peptides for inhibiting differentiation of progenitor
PT cells; also used for maintaining these cells in undifferentiated
PT state, e.g. for haematopoietic reconstitution
XX Claim 6; Fig 1A; 101pp; English.
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XX CC This is the amino acid sequence of human JAGGED1 (hJAGGED1), an
 CC activating ligand for Notch protein. hJAGGED1 is expressed in
 CC bone marrow stromal cells, and a stromal cell line expressing
 CC hJAGGED1 permits survival and proliferation of haematopoietic
 CC progenitor cells expressing Notch but inhibits granulocyte
 CC differentiation. A cDNA clone (see AAV63753) encoding hJAGGED1
 CC was obtained from a human bone marrow cDNA library. hJAGGED1
 CC polypeptides and biologically active peptides (see AA87896-98) are
 CC able (i) to inhibit differentiation of haematopoietic progenitor
 CC cells (HPC), e.g. for subsequent production of blood cells for
 CC transplantation or dendritic cells for immunotherapy, and (ii) to
 CC maintain HPC in the undifferentiated state, particularly totipotent
 CC cells or cells able to reconstitute the haematopoietic system e.g.
 CC in patients with leukemia or lymphoma. Treated HPC, e.g. where
 CC taken from a neonate, may be cryopreserved for many years, then
 CC thawed for further expansion and differentiation. Optionally
 CC Jagged may be provided by cells transformed to express the
 CC membrane-bound protein. Antibodies raised against hJAGGED1 can
 CC be used in a method of diagnosing Alagille syndrome by detecting
 CC reduced expression of hJAGGED1 or expression of abnormal hJAGGED1.
 XX CC
 SQ Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 20; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 1.3e-102;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 32 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
 QY 61 CSFGSGSTPVIGGNTFNFKASGRNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
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 DB 152 IEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
 QY 181 CDQNGNKTCEGWMGPEC 198
 DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 7
 ABB07822

ID ABB07822 standard; Protein; 1218 AA.
 XX ABB07822;
 XX
 XX 03-JUL-2002 (first entry)
 XX Human notch agonist ligand.
 XX
 XX Cell differentiation: notch; epidermis; cytostatic; dermatological;
 XX epithelial; skin; cancer; gamma secretase; human.
 XX Homo sapiens.
 XX
 XX WO200218544-A2.
 XX
 XX 07-MAR-2002.
 XX
 XX 31-AUG-2001; 2001WO-US27246.
 XX
 XX 31-AUG-2000; 2000US-229614P.
 XX
 XX (LOYO) UNIV LOYOLA CHICAGO.
 XX
 XX Nickoloff BJ, Miele L;
 XX WPI; 2002-339659/37.
 XX DR

XX PT Inducing differentiation of epithelial cell useful for inducing barrier
 PT information within epithelium for treating psoriasis, sunburn, involves
 PT exogenously providing a source of a Notch agonist to the epithelial
 PT cell -
 XX
 PS Claim 10; Page 76-81; 101pp; English.
 XX
 CC The invention relates to a method of inducing differentiation of
 CC at least one epithelial cell. The method involves exogenously providing
 CC at least one source of at least one Notch agonist to at least one
 CC epithelial cell, whereby the Notch pathway is activated within at least
 CC one epithelial cell so that the differentiation of the cell is induced.
 CC Methods of producing differentiated epidermis; for assaying for genetic
 CC propensity of a patient to develop a disorder associated with epithelial
 CC barrier formation; for retarding progression of skin cancer and for
 CC diagnosing aggressive melanoma are also provided. The methods are useful
 CC for inducing differentiation of at least one epithelial cell e.g. a
 CC keratinocyte or a pre-malignant cell, in vivo or ex vivo. The method is
 CC useful for inducing differentiation of epithelial cell within cutaneous
 CC epithelial tissue or dermal equivalent, or within extracutaneous
 CC epithelium such as oral mucosal epithelial tissue, cornea epithelial
 CC tissue, gastrointestinal epithelia, urogenital epithelia, or respiratory
 CC epithelia. The methods are useful retarding the progression of skin
 CC cancer such as aggressive melanoma, aggressive cutaneous T-cell lymphoma
 CC (CTCL), aggressive squamous cell carcinoma, or aggressive basal cell
 CC carcinoma, by preferably administering an antagonist of the Notch
 CC pathway such as gamma secretase inhibitor. The present sequence
 CC represents a human notch agonist ligand.
 XX
 SQ Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 23; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 1.3e-102;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
 DB 32 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
 QY 61 CSFGSGSTPVIGGNTFNFKASGRNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
 DB 92 CSFGSGSTPVIGGNTFNFKASGRNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 151
 QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
 DB 152 IEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
 QY 181 CDQNGNKTCEGWMGPEC 198
 DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 8
 ABB97800

ID ABB97800 standard; Protein; 1218 AA.
 XX ABB97800;
 XX
 XX 03-JUN-2003 (first entry)
 XX Amino acid sequence of human Jagged 1, a Notch ligand.
 XX
 XX MHC class II molecule; antigen presenting cell; APC; T cell;
 XX Notch signalling; T cell-mediated disease; tumour; autoimmune disorder;
 XX rheumatoid arthritis; graft rejection; asthma; HIV; multiple sclerosis;
 XX diabetes; hepatitis; cardiac disease; dermatitis; periodontal disease;
 XX reproductive disorder; Alzheimer's disease; Parkinson's disease;
 XX Huntington's disease; septic shock; stroke; Notch ligand; Jagged 1.
 XX Homo sapiens.
 XX
 XX WO2003012111-A2.
 XX PN

PT Notch signalling in a cell of the immune system in the presence of
XX modulator
XX
PS Disclosure; Fig 34; 184pp; English.

CC The present sequence is the protein sequence of the human Notch
XX ligand, Jagged 1. Jagged 1, its fragment, derivative, homologue,
CC analogue or allelic variant, or a polynucleotide encoding it,
CC can be used as a modulator of the Notch signalling pathway in the
CC method of the invention. The modulator may also comprise the Delta
CC Serrate lag2 (DSL) domain and at least one of the EGF-like repeat
CC motifs of a Notch ligand. The method detects modulators of Notch
CC signalling by monitoring the effect of a candidate modulator on
CC Notch signalling in a cell of the immune system, such as a T cell,
CC a B cell or an antigen presenting cell. The method is useful for
CC preparing a medicament for treating a disease or condition of, or
CC related to, the immune system, such as T-cell, B-cell or APC
CC mediated disease (all claimed), including cancer, acute and chronic
CC immune and autoimmune pathologies, infectious diseases,
CC inflammatory diseases, neurodegenerative diseases, alcohol-induced
CC hepatitis, other diseases related to angiogenesis, cardiovascular
CC conditions and pulmonary diseases.

XX Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 24; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILLSMQNVNGLQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 32 SQGFLEILLSMQNVNGLQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 91
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CSFGSGSTPVIGGNTNFKASRGNDNRNIRVLPFSFAPRPSYTLVVEAWSSNDTVQDPSI 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 92 CSFGSGSTPVIGGNTNFKASRGNDNRNIRVLPFSFAPRPSYTLVVEAWSSNDTVQDPSI 151
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 211
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 CDQNGNKTCEGWMGPEC 198
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 212 CDQNGNKTCEGWMGPEC 229

RESULT 10

AAE34031
ID AAE34031 standard; Protein; 1218 AA.

XX AAE34031;

XX 02-MAY-2003 (first entry)

XX Human notch ligand jagged 1 protein.

XX Human; drug screening; toxicology assay; signalling pathway;

XX notch ligand jagged 1; JAG1 protein.

XX Homo sapiens.

XX WO200290992-A2.

XX 14-NOV-2002.

XX 29-APR-2002; 2002WO-GB01946.

XX 04-MAY-2001; 2001GB-0011004.

XX (AXOR-) AXORDIA LTD.

XX Andrews P, Draper J, Walsh J;

DR WPI; 2003-120579/11.
XX N-PSDB; AAD52525.

XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested,
PT and detecting signals generated by a reporter molecule as a result of
XX exposure to the agent
XX
PS Claim 16; Fig 5; 90pp; English.

XX The present invention relates to a novel screening method which enables
CC the identification of biologically active agents which mediate their
CC effect through the activation of genes. The method involves providing a
CC population of cells stably transfected with a nucleic acid encoding a
CC reporter molecule, cloning the transfected cells into a cell array,
CC exposing the array to at least one agent to be tested and detecting a
CC signal generated by the reporter molecule as a result of exposure to
CC the agent. The method is useful in identifying biologically active agents
CC and the genes through which the agents act, in screening potential drugs
CC for their ability to activate certain drug targets in a high-throughput
CC assay, in identifying relationships between signalling pathways and
CC specific signals that could be useful in eventually directing the
CC differentiation of embryonic stem cells and in toxicology assays by
CC testing for unwanted activation or inhibition of specific signalling
CC pathways. The present sequence is human notch ligand jagged 1 (JAG1)
CC protein used to illustrate the method of the invention.
CC Note: This sequence is encoded by a DNA containing translation
CC exceptions which alter the reading frame.

XX Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 24; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILLSMQNVNGLQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 32 SQGFLEILLSMQNVNGLQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 91
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CSFGSGSTPVIGGNTNFKASRGNDNRNIRVLPFSFAPRPSYTLVVEAWSSNDTVQDPSI 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 92 CSFGSGSTPVIGGNTNFKASRGNDNRNIRVLPFSFAPRPSYTLVVEAWSSNDTVQDPSI 151
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 211
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 CDQNGNKTCEGWMGPEC 198
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 212 CDQNGNKTCEGWMGPEC 229

RESULT 11

ABU55874
ID ABU55874 standard; Protein; 1218 AA.

XX ABU55874;

XX 25-MAR-2003 (first entry)

XX Human notch ligand jagged 1 Protein.

XX Notch; Wnt; embryonic stem cell; embryogenesis; human;
KW differentiation; ligand; Parkinson's disease; Huntington's disease;
KW motor neuron disease; heart disease; diabetes; liver disease;
KW cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens..

XX WO200277204-A2.

XX 03-OCT-2002.

25-MAR-2002; 2002WO-GB011195.
23-MAR-2001; 2001GB-0007296.
23-MAR-2001; 2001GB-0007299.
17-APR-2001; 2001GB-0009346.
(AXOR-) AXORDIA LTD.
Andrews P, Walsh J, Gokhale P;
WPI; 2003-092852/08.
N-PSDB; ABX75298.
Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful for treating diseases such as Parkinson's, Huntington's, heart disease, diabetes and AIDS
Claim 6; Fig 6; 121pp; English.
The invention relates to modulating the differentiation of an embryonic stem cell, comprising: (a) providing a culture of embryonic stem cells; (b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cell; (c) forming a culture comprising embryonic stem cells and the ligand; and (d) growing the cell culture. Also included are: (1) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic acid molecule that hybridises to the nucleic acid in (i), and which encodes a ligand capable of modulating embryonic stem cell differentiation, or capable of binding a Wnt receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance and/or differentiation of the embryonic stem cell; (2) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing at least one polypeptide or its active fragment, that are inhibitors of the Wnt signalling pathway; (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; or (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises to the molecule of (i) and encodes a polypeptide capable of inhibiting Wnt signalling; and (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; and (4) A cell, therapeutic cell or cell culture obtainable by any of the methods cited above.
The therapeutic cell of the present invention is useful in the treatment of an animal, preferably a human, comprising administering a cell composition comprising embryonic stem cells which have been induced to differentiate into at least one cell-type. The cell is also useful for the manufacture of a composition for use in treatment of diseases such as Parkinson's disease, Huntington's disease, motor neuron disease, heart disease, diabetes, liver disease (e.g. cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome). The present sequence is represents a Wnt or Notch pathway protein (i.e. a ligand for the method of the invention).

Sequence 1218A;

Query Match 100.0%; Score 1116; DB 24; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SQOFFEILSMQNVGELQNGCCGARNPCDRKTRDECPTYKVLKEYQSRVTAGGP 60
|||||
32 SQOFFEILSMQNVGELQNGCCGARNPCDRKTRDECPTYKVLKEYQSRVTAGGP 91

QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAWPRSYTLLEAMDSNDTVQPD SI 120
DB 92 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAWPRSYTLLEAMDSNDTVQPD SI 151
QY 121 IEKASHSGMINP SROWQTLKQNTGVAHFEYQIRVTCDDYYYGFGNCKFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINP SROWQTLKQNTGVAHFEYQIRVTCDDYYYGFGNCKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEMGWGP EC 198
DB 212 CDQNGNKTCEMGWGP EC 229

RESULT 12

ABP97797
ID ABP97797 standard; Protein: 296 AA.

AC ABP97797;

DT 03-JUN-2003 (first entry)

DE Amino acid sequence of human Jagged 1 (hJagl) fragment.

KW MHC class II molecule; antigen presenting cell; APC; T cell;
KW Notch signalling; T cell-mediated disease; tumour; autoimmune disorder;
KW rheumatoid arthritis; graft rejection; asthma; HIV; multiple sclerosis;
KW diabetes; hepatitis; cardiac disease; dermatitis; periodontal disease;
KW reproductive disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; septic shock; stroke; Notch ligand; Jagged 1.

OS Homo sapiens.

PN WO2003012111-A2.

PD 13-FEB-2003.

PF 25-JUL-2002; 2002WO-GB03381.

PR 25-JUL-2001; 2001GB-0018155.

PA (LORA-) LORANTIS LTD.

PI Bodmer MW, Champion BR, McKenzie GU, Nye LE;

DR WPI: 2003-278403/27.

PT New conjugate, useful for treating T cell-mediated disease e.g. tumours
PT or autoimmune disorders, comprises a polypeptide capable of binding to
PT an antigen presenting cell and a polypeptide capable of modulating a T
PT cell signalling pathway -

PS Example 1; Page 67; 93pp; English.

CC The specification describes a conjugate, comprising first and second
CC sequences, where the first sequence comprises a polypeptide which is
CC capable of binding to a MHC class II molecule (e.g., on an antigen
CC presenting cell (APC)), and the second sequence comprises a polypeptide
CC capable of modulating a T cell signalling pathway (e.g. a protein for
CC Notch signalling transduction). The conjugate is useful for preparing a
CC composition for treating or preventing T cell-mediated disease,
CC e.g. tumours, autoimmune disorders such as rheumatoid arthritis, graft
CC rejection, asthma, HIV, multiple sclerosis, diabetes, hepatitis, cardiac
CC diseases, dermatitis, periodontal diseases, reproductive disorders,
CC Alzheimer's disease, Parkinson's disease, Huntington's disease, septic
CC shock and stroke. The present sequence represents a fragment of human
CC jagged 1 (hJagl). hJagl is a Notch ligand, which may act as the second
CC polypeptide in conjugates of the invention.

SQ Sequence 296 AA;

Query Match 99.4%; Score 1109; DB 24; Length 296;
Best Local Similarity 99.5%; Pred. No. 1e-102;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
QY 1 SQQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSSI 120
Db 92 CSFGSGSTPVIGGNTFNKASRGNDNRNIRVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSSI 151
QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYYGFCNKFCRPRDDFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYYGFCNKFCRPRDDFGHYA 211
QY 181 CDQNGNKTCTMEGWMGPCC 198
Db 212 CDQNGNKTCTMEGWMGPCC 229

RESULT 13
AAW05833
ID AAW05833 standard; Protein; 1218 AA.
XX AC AAW05833;
XX 25-MAR-2003 (updated)
DT 28-JAN-1997 (first entry)
XX DE Human Serrate-1 (HJ1).
XX KW Serrate-1; human jagged-1; HJ1; Notch; cell differentiation;
KW cell fate; central nervous system; cancer; tissue repair; therapy;
KW diagnosis; antibody.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Domain 1..1067
FH Peptide 14..29
FH Domain 185..229
FH /label= DSL
FH /note= "region of homology with Drosophila Delta
FH and Serrate, predicted to mediate binding
FH with Notch"
FH Domain 234..896
FH /label= ELR
FH /note= "epidermal growth factor-like repeat domain"
FH Region 234..264
FH /label= ELR1
FH Region 265..299
FH /label= ELR2
FH Region 300..339
FH /label= ELR3
FH Region 340..377
FH /label= ELR4
FH Region 378..415
FH /label= ELR5
FH Region 416..453
FH /label= ELR6
FH Region 454..490
FH /label= ELR7
FH Region 491..528
FH /label= ELR8
FH Region 529..566
FH /label= ELR9
FH Region 567..598
FH /label= Partial_ELRL
FH Region 599..632
FH /label= Partial_ELRL
FH Region 633..670
FH /label= ELR10
FH Region 671..708
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FT Region /label= ELRL1
FT 709..747
FT /label= ELRL2
FT Region 748..785
FT /label= ELRL3
FT Region 786..823
FT /label= ELRL4
FT Region 824..862
FT /label= ELRL5
FT Region 863..879
FT /label= Partial_ELRL
FT Region 880..896
FT /label= Partial_ELRL
FT Domain 1068..1089
FT /label= Transmembrane_domain
FT Domain 1090..1218
FT /label= Intracellular_domain
XX XX
PN WO9627610-A1.
XX 12-SEP-1996.
XX PF 07-MAR-1996; 96WO-US03172.
XX PR 07-MAR-1995; 95US-0400159.
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA (UYIA ) UNIV YALE.
XX Ishhorowicz D, Henrique DMP, Lewis JH, Myat AM;
PI Artavanis-tsakonas S, Mann RS, Gray GE;
XX WPI; 1996-425379/42.
DR N-PSDB; AAT40090.
XX Vertebrate Serrate protein and related DNA - used to treat or
PT prevent malignancies characterised by increased Notch activity.
PS Claim 4; Page 95-98; 16lpp; English.
XX Human Serrate-1 (AAW05833) and human Serrate-2 (AAW05833) are ligands
CC for the zygotic neurogenic locus Notch, and are believed to play a
CC major role in determining cell fates (differentiation) in the
CC central nervous system. Their amino acid sequences were deduced
CC from cDNA clones (see also AAT40090-91) isolated from human foetal
CC brain cDNA libraries. The proteins, antibodies raised to them,
CC and encoding nucleic acids can be used in the detection of
CC Serrate sequences and in the treatment of disorders of cell fate
CC or differentiation, partic. cancer, nervous system disorders
CC and in tissue repair or regeneration.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 1218 AA;
Query Match 99.4%; Score 1109; DB 17; Length 1218;
Best Local Similarity 99.5%; Pred. No. 6.4e-102;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SQQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSSI 120
Db 92 CSFGSGSTPVIGGNTFNKASRGNDNRNIRVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSSI 151
QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYYGFCNKFCRPRDDFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYYGFCNKFCRPRDDFGHYA 211
QY 181 CDQNGNKTCTMEGWMGPCC 198
Db 212 CDQNGNKTCTMEGWMGPCC 229
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RESULT 14	
AA59597	
ID	AA59597 standard; Protein; 1218 AA.
XX	AC
XX	AA59597;
XX	05-APR-2000 (first entry)
DT	XX
XX	Human Serrate protein sequence.
DE	XX
KW	Serrate; cancerous condition; melanoma; lung cancer; breast cancer;
KW	nervous system disorder; infection; nutritional disease; therapy;
KW	cell proliferation promoter; tissue regeneration; human.
XX	XX
OS	Homo sapiens.
XX	XX
PN	US6004924-A.
XX	XX
PD	21-DEC-1999.
XX	XX
XX	06-MAR-1996; 96US-0611729.
PR	11-DEC-1991; 91US-0808458.
PR	14-SEP-1993; 93US-0121979.
PR	07-JUN-1994; 94US-0255102.
PR	07-MAR-1995; 95US-0400159.
XX	XX
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA	(UYVA) UNIV YALE.
PI	Ish-Horowicz D, Henrique DMP, Myat AM, Fleming RJ;
PI	Artavanis-Tsakonas S, Gray GE, Mann RS, Lewis JH;
XX	XX
DR	WPI; 2000-105089/09.
DR	N-PSDB; AA249096.
PT	Purified Serrate proteins useful for treating neoplasias, nervous
PT	disorders and for promoting cell proliferation and tissue regeneration
PT	and repair
XX	XX
PS	Claim 1; Fig 9; 114pp; English.
XX	XX
CC	This sequence represents a human serrate protein.
CC	The invention relates to purified vertebrate (mouse, chick, and human)
CC	Serrate proteins. The Serrate proteins may be administered to treat a
CC	cancerous condition (e.g. melanoma, lung cancer and breast cancer) by
CC	preventing progression from a preneoplastic or nonmalignant state into a
CC	neoplastic or malignant state. It may also be used to treat nervous
CC	system disorders (such as lesions caused by infections, nutritional
CC	disease and toxic substances) and to promote cell proliferation and
CC	tissue regeneration and repair. The protein itself is administered to
CC	suppress a patient's own production of Serrate proteins (if levels of
CC	expression are low) or to compensate for expression of inactive proteins
CC	due to genetic mutations. The protein may also be used in the production
CC	of antibodies against Serrate proteins which may be used to either down
CC	regulate Serrate activity or to detect Serrate proteins in samples (for
CC	example via enzyme-linked immunosorbant assay (ELISA)). The proteins may
CC	also be used to study Serrate expression and its role in metabolism and
CC	to assay for agents which modulate its expression and activity.
XX	XX
SQ	Sequence 1218 AA;
Query Match	99.4%; Score 1109; DB 21; Length 1218;
Best Local Similarity	99.5%; Pred. No. 6.4e-102;
Matches 197; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 SQQFEILSMQNVNGLQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 60
DB	32 SQQFEILSMQNVNGLQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 91
QY	61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120
DB	92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 151
QY	121 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 180
DB	152 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFGHYA 211
QY	181 CDQNGNKTCEMGWGMEC 198
DB	212 CDQNGNKTCEMGWGMEC 229
RESULT 15	
AA084344	
ID	AA084344 standard; Protein; 1218 AA.
XX	AC
XX	AA084344;
DT	08-MAY-2002 (first entry)
XX	XX
XX	Protein JAG1 differentially expressed in breast cancer tissue.
DE	XX
KW	Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW	MAI; mitotic activity index; cytostatic.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO200210436-A2.
XX	XX
PD	07-FEB-2002.
XX	XX
PF	27-JUL-2001; 2001WO-US23642.
XX	XX
XX	28-JUL-2000; 2000US-222093P.
XX	XX
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA	(BAAK/) BAAK J.
XX	XX
PI	Baak J, Mutter GL;
XX	XX
DR	WPI; 2002-180084/23.
DR	N-PSDB; ABK35564.
PT	Diagnosing breast cancer comprises determining expression of nucleic
PT	acid molecules or expression products that are differentially expressed
PT	in normal and malignant tissue
XX	XX
PS	Claim 37; Page 163-167; 219pp; English.
XX	XX
CC	The present invention relates to a method for diagnosing breast cancer
CC	in a subject suspected of having endometrial cancer. The method
CC	comprises determining the expression of a set of human genes or
CC	expression products in an endometrial sample suspected of being
CC	cancerous. The human genes of the invention are differentially
CC	expressed in breast tumours characterised as high or low MAI (mitotic
CC	activity index). These sets of genes can be used to discriminate between
CC	high and low MAI breast tumours. The invention also provides DNA and
CC	protein microarrays for analysing the expression of the human genes and
CC	their protein products. The methods and arrays are useful for the
CC	diagnosis and prognosis of endometrial cancer, selecting and monitoring
CC	treatment regimes, and identification of compounds useful for the
CC	treatment of endometrial cancer. AA084311-AA084361 represent the human
CC	proteins of the invention that are differentially expressed in breast
CC	cancer tissue.
XX	XX
SQ	Sequence 1218 AA;
Query Match	99.4%; Score 1109; DB 23; Length 1218;
Best Local Similarity	99.5%; Pred. No. 6.4e-102;
Matches 197; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 SQQFEILSMQNVNGLQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 60
DB	32 SQQFEILSMQNVNGLQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 91
QY	61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120

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Db      32 SGOFELEILSMQNVNGLQNGCCGARNPGRKTRDECDTYFKVCLKEYQSRVTAGGP 91
Qy      61 CSFGSGSTPVIGNTFNLKASRGNDNRNRIVLPEFAWPRSYTLLVEAWDSSNDTVQPD SI 120
Db      92 CSFGSGSTPVIGNTFNLKASRGNDNRNRIVLPEFAWPRSYTLLVEAWDSSNDTVQPD SI 151
Qy     121 IEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db     152 IEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
Qy     181 CDQNGNKTCMEGWMGPEC 198
Db     212 CDQNGNKTCMEGWMGPEC 229

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Search completed: August 25, 2003, 17:52:28
 Job time : 87 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:50:58 ; Search time 30 Seconds
(without alignments)
279.252 Million cell updates/sec

Title: US-09-995-593A-5

Perfect score: 1116

Sequence: 1 SQQFEILSMQNVGELQN.....YACDQNGKTCMEGWGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1116	100.0	198	4	US-09-068-740A-5
2	1116	100.0	1010	3	US-08-882-046-7
3	1116	100.0	1036	4	US-09-068-740A-6
4	1116	100.0	1187	4	US-09-068-740A-7
5	1116	100.0	1218	3	US-08-882-046-2
6	1116	100.0	1218	4	US-09-068-740A-11
7	1109	99.4	1208	4	US-09-199-865-1
8	1109	99.4	1218	2	US-08-400-159-6
9	1109	99.4	1218	3	US-08-611-729A-6
10	1109	99.4	1219	3	US-08-882-046-5
11	1106	99.1	1218	3	US-09-214-278-7
12	970	86.9	1193	2	US-08-400-159-10
13	970	86.9	1248	3	US-08-611-729A-10
14	653	58.5	1248	3	US-08-882-046-6
15	652	58.4	214	3	US-09-214-278-1
16	652	58.4	1055	3	US-09-214-278-2
17	652	58.4	1212	3	US-09-214-278-3
18	652	58.4	1238	3	US-09-214-278-5
19	584.5	52.4	1148	3	US-08-882-046-4
20	446	40.0	293	1	US-08-264-534-9
21	446	40.0	293	1	US-08-083-590A-4
22	446	40.0	293	1	US-08-465-500-9
23	446	40.0	293	2	US-08-346-126-9
24	446	40.0	293	2	US-08-346-128-9
25	446	40.0	293	3	US-08-532-384-4
26	446	40.0	293	3	US-08-893-828-9
27	446	40.0	1404	2	US-08-400-159-2

28 446 40.0 1404 3 US-08-611-729A-2 Sequence 2, Appli
29 445 39.9 199 1 US-08-264-534-4 Sequence 4, Appli
30 445 39.9 199 1 US-08-465-500-4 Sequence 4, Appli
31 445 39.9 199 2 US-08-346-126-4 Sequence 4, Appli
32 445 39.9 199 2 US-08-346-128-4 Sequence 4, Appli
33 445 39.9 199 3 US-08-893-828-4 Sequence 2, Appli
34 433.5 38.8 728 3 US-08-981-392-2 Sequence 8, Appli
35 433.5 38.8 729 3 US-08-872-855-8 Sequence 3, Appli
36 431 38.6 520 4 US-09-068-740A-3 Sequence 9, Appli
37 431 38.6 702 4 US-09-068-740A-4 Sequence 9, Appli
38 431 38.6 723 4 US-08-400-159-4 Sequence 4, Appli
39 423 37.9 236 2 US-08-611-729A-4 Sequence 11, Appli
40 423 37.9 236 3 US-08-872-855-11 Sequence 6, Appli
41 423 37.9 830 3 US-08-284-534-6 Sequence 6, Appli
42 423 37.9 833 1 US-08-083-590A-2 Sequence 6, Appli
43 423 37.9 833 1 US-08-465-500-6 Sequence 6, Appli
44 423 37.9 833 1 US-08-346-126-6
45 423 37.9 833 2

ALIGNMENTS

RESULT 1

US-09-068-740A-5

; Sequence 5, Application US/09068740A

; Patent No. 6337387

; GENERAL INFORMATION:

; APPLICANT: SAKANO, SEIJI

; APPLICANT: ITOH, AKIRA

; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

; FILE REFERENCE: KP-8447

; CURRENT APPLICATION NUMBER: US/09/068,740A

; CURRENT FILING DATE: 1998-06-18

; PRIOR FILING DATE: 1995-11-17

; PRIOR FILING DATE: 1995-11-17

; PRIOR FILING DATE: 1995-11-30

; PRIOR APPLICATION NUMBER: PCT/JP96/03356

; PRIOR FILING DATE: 1996-11-15

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 198

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-068-740A-5

Query Match 100.0%; Score 1116; DB 4; Length 198;

Best Local Similarity 100.0%; Pred. No. 3e-110;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQQFEILSMQNVGELQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60

Db 1 SQQFEILSMQNVGELQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60

Qy 61 CSFGSGSTPYIGGNTFNKASRGNDNRIVLPFSFAMPRSYTLLVEAWDSNDTVQPD SI 120

Db 61 CSFGSGSTPYIGGNTFNKASRGNDNRIVLPFSFAMPRSYTLLVEAWDSNDTVQPD SI 120

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180

Db 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180

Qy 181 CDQNGKTCMEGWGPEC 198

Db 181 CDQNGKTCMEGWGPEC 198

RESULT 2

US-08-882-046-7

; Sequence 7, Application US/08882046

; Patent No. 6136952

GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spiner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1010 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-882-046-7

Query Match 100.0%; Score 1116; DB 3; Length 1010;
Best Local Similarity 100.0%; Pred. No. 2.5e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 32 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
|||||

QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 120
|||||

Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 151
|||||

QY 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
|||||

Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
|||||

QY 181 CDQNGKNTCMEGWMGPEC 198
|||||

Db 212 CDQNGKNTCMEGWMGPEC 229
|||||

RESULT 3
US-09-068-740A-6
Sequence 6, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING DATE: 1995-11-17

PRIOR APPLICATION NUMBER: JP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1036
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-6

Query Match 100.0%; Score 1116; DB 4; Length 1036;
Best Local Similarity 100.0%; Pred. No. 2.6e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||

QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 120
|||||

Db 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 120
|||||

QY 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
|||||

Db 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
|||||

QY 181 CDQNGKNTCMEGWMGPEC 198
|||||

Db 181 CDQNGKNTCMEGWMGPEC 198
|||||

RESULT 4
US-09-068-740A-7
Sequence 7, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: JP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1187
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-7

Query Match 100.0%; Score 1116; DB 4; Length 1187;
Best Local Similarity 100.0%; Pred. No. 3.1e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||

Db 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||

QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 120
|||||

Db 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYYTLVAVDSSNDTVQPSI 120
|||||

QY 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
|||||

Db 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
|||||

Oy 181 CDQNGKTCMEGWMGPEC 198
Db 181 CDQNGKTCMEGWMGPEC 198

RESULT 5

US-08-882-046-2
; Sequence 2, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Krantz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-882-046-2

Query Match 100.0%; Score 1116; DB 3; Length 1218;
Best Local Similarity 100.0%; Pred. No. 3.3e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGOFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SGOFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
Oy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYTLTLLVEAWDSSNDTVOPDSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYTLTLLVEAWDSSNDTVOPDSI 151
Oy 121 IEKASHGMINPSPROWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSPROWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
Oy 181 CDQNGKTCMEGWMGPEC 198
Db 212 CDQNGKTCMEGWMGPEC 229

RESULT 6

US-09-068-740A-11
; Sequence 11, Application US/09068740A

; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-11

Query Match 100.0%; Score 1116; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 3.3e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGOFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SGOFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
Oy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYTLTLLVEAWDSSNDTVOPDSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPSFAWPRSYTLTLLVEAWDSSNDTVOPDSI 151
Oy 121 IEKASHGMINPSPROWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSPROWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
Oy 181 CDQNGKTCMEGWMGPEC 198
Db 212 CDQNGKTCMEGWMGPEC 229

RESULT 7

US-09-199-865-1
; Sequence 1, Application US/09199865
; Patent No. 6433138
; GENERAL INFORMATION:

; APPLICANT: Zimrin, Ann B.
; APPLICANT: Maciag, Thomas
; APPLICANT: Wong, Michael K.K.
; APPLICANT: Pepper, Michael S.
; APPLICANT: Montesano, Roberto
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 0036-101
; CURRENT APPLICATION NUMBER: US/09/199,865
; CURRENT FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: 60/018,841
; EARLIER FILING DATE: 1996-05-31
; EARLIER APPLICATION NUMBER: PCT/US97/09407
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-199-865-1

Query Match 99.4%; Score 1109; DB 4; Length 1208;
Best Local Similarity 99.5%; Pred. No. 1.8e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 60
DB 22 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 81
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 120
DB 82 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 141
QY 121 TEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYYYGFGCNKFCRPRDDFFGHYA 180
DB 142 TEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYYYGFGCNKFCRPRDDFFGHYA 201
QY 181 CDQNGNKTCMEGWMGPEC 198
DB 202 CDQNGNKTCMEGWMGPEC 219

RESULT 8

US-08-400-159-6
; Sequence 6, Application US/08400159
; Patent No. 5869282
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,159
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-400-159-6

Query Match 99.4%; Score 1109; DB 2; Length 1218;
Best Local Similarity 99.5%; Pred. No. 1.8e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 60
DB 32 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 91

QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 120
DB 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 151
QY 121 TEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYYYGFGCNKFCRPRDDFFGHYA 180
DB 152 TEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCMEGWMGPEC 198
DB 212 CDQNGNKTCMEGWMGPEC 229

RESULT 9

US-08-611-729A-6
; Sequence 6, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,729A
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1218 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-611-729A-6

Query Match 99.4%; Score 1109; DB 3; Length 1218;
Best Local Similarity 99.5%; Pred. No. 1.8e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 60
DB 32 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 120
DB 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPDISI 151

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 211
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Qy 181 CDQNGKTCMEGWMGPEC 198
|||||
Db 212 CDQNGKTCMEGWMGPEC 229
|||||

RESULT 10

US-08-882-046-5
; Sequence 5, Application US/08882046
; Patent No. 6136952

GENERAL INFORMATION:

APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/882.046

FILING DATE: 25-JUN-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UW 2637

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:

LENGTH: 1219 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-882-046-5

Query Match 99.4%; Score 1109; DB 3; Length 1219;
Best Local Similarity 98.5%; Pred. No. 1.8e-108;
Matches 195; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQQFEILSMQNVNGELQNGCCGARNFGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 32 SQQFEILSMQNVNGELQNGCCGARNFGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 91
|||||
Qy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120
|||||
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 151
|||||

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 211
|||||

Qy 181 CDQNGKTCMEGWMGPEC 198
|||||

Db 212 CDQNGKTCMEGWMGPEC 229
|||||

RESULT 11

US-09-214-278-7
; Sequence 7, Application US/09214278
; Patent No. 6291210

GENERAL INFORMATION:

APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214.278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens

US-09-214-278-7

Query Match 99.1%; Score 1106; DB 3; Length 1218;
Best Local Similarity 99.5%; Pred. No. 3.7e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQQFEILSMQNVNGELQNGCCGARNFGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 32 SQQFEILSMQNVNGELQNGCCGARNFGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 91
|||||
Qy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120
|||||
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 151
|||||

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 211
|||||

Qy 181 CDQNGKTCMEGWMGPEC 198
|||||

Db 212 CDQNGKTCMEGWMGPEC 229
|||||

RESULT 12

US-08-400-159-10
; Sequence 10, Application US/08400159
; Patent No. 5869282

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,159

FILING DATE: 07-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-159-10

Query Match 86.9%; Score 970; DB 2; Length 1193;
Best Local Similarity 84.8%; Pred. No. 8.7e-94;
Matches 168; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1 SQFELEILSMQNVGELONGCCGARNPGDKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 6 SQFELEILSVQNVGVQNGCCDTRNPGDKKCTRDECDTYFKVCLKEYQSRVTAGGP 65
QY 61 CSFGSGSTPVGIGNTFNKASRGNDNRNRIPLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 120
DB 66 CSFGSKSTPVGIGNTFNKASRNNEKNRIVIPPTFAWPRSYLLVEAWDYNNDSTNPDR I 125
QY 121 IEKASHGMINPSRQWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDRDFFGHYA 180
DB 126 IEKASHGMINPSRQWQTLKHTNTGAHFEYQIRVTCAEHYGFGCNKFCRPRDRDFFTHHT 185
QY 181 CDQNGNKTCEGMWGPEC 198
DB 186 CDQNGNKTCEGWGTGPEC 203

RESULT 13
US-08-611-729A-10
Sequence 10, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-611-729A-10

Query Match 86.9%; Score 970; DB 3; Length 1193;
Best Local Similarity 84.8%; Pred. No. 8.7e-94;
Matches 168; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1 SQFELEILSMQNVGELONGCCGARNPGDKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 6 SQFELEILSVQNVGVQNGCCDTRNPGDKKCTRDECDTYFKVCLKEYQSRVTAGGP 65
QY 61 CSFGSGSTPVGIGNTFNKASRGNDNRNRIPLPFSFAPRSTYLLVEAWDSSNDTVQPD SI 120
DB 66 CSFGSKSTPVGIGNTFNKASRNNEKNRIVIPPTFAWPRSYLLVEAWDYNNDSTNPDR I 125
QY 121 IEKASHGMINPSRQWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDRDFFGHYA 180
DB 126 IEKASHGMINPSRQWQTLKHTNTGAHFEYQIRVTCAEHYGFGCNKFCRPRDRDFFTHHT 185
QY 181 CDQNGNKTCEGMWGPEC 198
DB 186 CDQNGNKTCEGWGTGPEC 203

RESULT 14
US-08-882-046-6
Sequence 6, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-882-046-6

Query Match 58.5%; Score 653; DB 3; Length 1248;
Best Local Similarity 56.5%; Pred. No. 3.1e-60;
Matches 121; Conservative 27; Mismatches 48; Indels 18; Gaps 5;

QY 2 GQFELEILSMQNVGELQNGNCC-GGARPNPGRKTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 28 GYFELQLSALRNVNGELLSGACCDGGRTRAGCGGDECDTYVRVCLKEYQAKVTPTGP 87
QY 61 CSFGSGSTPVIGGNTNL-KASRGNDNR-----IVLPFSFAMPRSYTLIVE 106
DB 88 CSYGGATPVLGNSFYLPAGAAGDRARARSRTGGHODPLVVIPIPFQFAMPRSFLLIVE 147
QY 107 AWDSSNDTVQPDSS--IIEKASHSGMINPSQWOTLKQNTGVAHFEYQIRVTCDDYYGFG 164
DB 148 AWDNDNTT-PDELLIERVSHAGMINPEDRWKSLHFSGHVAHLELQIRVRCDENYSATC 206
QY 165 CNKFCRPRDFFGHYACDQNGKTCMEGWMGPEC 198
DB 207 CNKFCRPRDFFGHYTCDOYGNKACMDGWMGKEC 240

RESULT 15

US-09-214-278-1
; Sequence 1; Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-278-1

Query Match 58.4%; Score 652; DB 3; Length 214;
Best Local Similarity 55.4%; Pred. No. 3.9e-61;
Matches 118; Conservative 31; Mismatches 48; Indels 16; Gaps 4;

QY 2 GQFELEILSMQNVGELQNGNCC-GGARPNPGRKTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 2 GYFELQLSALRNVNGELLSGACCDGGRTRAGCGGDECDTYVRVCLKEYQAKVTPTGP 61
QY 61 CSFGSGSTPVIGGNTNL-----KASRGNDNR--RIVLPFSFAMPRSYTLIVE 106
DB 62 CSYGGATPVLGNSFYLPAGAAGDRARARAGGQDPLVVIPIPFQFAMPRSFLLIVE 121
QY 107 AWDSSNDTV-QPDSIIEKASHSGMINPSQWOTLKQNTGVAHFEYQIRVTCDDYYGFGC 165
DB 122 AWDNDNTT-PDELLIERVSHAGMINPEDRWKSLHFSGHVAHLELQIRVRCDENYSATC 181
QY 166 NKFCRPRDFFGHYACDQNGKTCMEGWMGPEC 198
DB 182 NKFCRPRDFFGHYTCDOYGNKACMDGWMGKEC 214

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Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2003, 17:52:33 ; Search time 57 Seconds
(without alignments)
458.393 Million cell updates/sec

Title: US-09-995-593A-5
Perfect score: 1116
Sequence: 1 SQGFELLSQNVNGELQN.....YACDQNGKTCMEGWMGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues .

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	198	US-09-995-593A-5	Sequence 5, Appli
2	1116	100.0	1036	US-09-995-593A-6	Sequence 6, Appli
3	1116	100.0	1187	US-09-995-593A-7	Sequence 7, Appli
4	1116	100.0	1218	US-09-995-593A-11	Sequence 11, Appli
5	1116	100.0	1218	US-09-944-849-3	Sequence 3, Appli
6	1109	99.4	1208	US-10-213-329-1	Sequence 1, Appli
7	1106	99.1	1218	US-09-855-722-7	Sequence 7, Appli
8	1106	99.1	1218	US-10-219-248-7	Sequence 7, Appli
9	1106	99.1	1218	US-10-219-247-7	Sequence 7, Appli
10	1102	98.7	1218	US-10-281-478-7	Sequence 7, Appli
11	652	58.4	214	US-09-855-722-1	Sequence 1, Appli
12	652	58.4	214	US-10-219-248-1	Sequence 1, Appli
13	652	58.4	214	US-10-219-247-1	Sequence 1, Appli
14	652	58.4	1055	US-09-855-722-2	Sequence 2, Appli
15	652	58.4	1055	US-10-219-248-2	Sequence 2, Appli

16	652	58.4	1055	15	US-10-219-247-2	Sequence 2, Appli
17	652	58.4	1212	9	US-09-855-722-3	Sequence 3, Appli
18	652	58.4	1212	15	US-10-219-248-3	Sequence 3, Appli
19	652	58.4	1212	15	US-10-219-247-3	Sequence 3, Appli
20	652	58.4	1238	9	US-09-855-722-5	Sequence 5, Appli
21	652	58.4	1238	10	US-09-944-849-4	Sequence 4, Appli
22	652	58.4	1238	15	US-10-219-248-5	Sequence 5, Appli
23	652	58.4	1238	15	US-10-219-247-5	Sequence 5, Appli
24	446	40.0	1404	10	US-09-944-849-8	Sequence 8, Appli
25	433.5	38.8	728	10	US-09-908-322-2	Sequence 2, Appli
26	433.5	38.8	728	11	US-09-783-931-2	Sequence 2, Appli
27	431	38.6	520	10	US-09-995-593A-3	Sequence 3, Appli
28	431	38.6	702	10	US-09-995-593A-4	Sequence 4, Appli
29	431	38.6	723	9	US-09-828-366-21	Sequence 21, Appli
30	431	38.6	723	10	US-09-995-593A-9	Sequence 9, Appli
31	431	38.6	723	12	US-10-137-870-346	Sequence 346, App
32	431	38.6	723	12	US-10-140-018-346	Sequence 346, App
33	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
34	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
35	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
36	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
37	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
38	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
39	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
40	431	38.6	723	12	US-10-141-698-346	Sequence 346, App
41	431	38.6	723	12	US-10-141-702-346	Sequence 346, App
42	431	38.6	723	12	US-10-141-704-346	Sequence 346, App
43	431	38.6	723	12	US-10-142-421-346	Sequence 346, App
44	431	38.6	723	12	US-10-142-432-346	Sequence 346, App
45	431	38.6	723	12	US-10-142-767-346	Sequence 346, App

ALIGNMENTS

RESULT 1
US-09-995-593A-5
; Sequence 5, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP-7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-5

Query Match .100.0%; Score 1116; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.4e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFELLSQNVNGELQNGCGARNPGDKTRDECDFYFKVCLKEYSRVTAGCP 60
DB 1 SQGFELLSQNVNGELQNGCGARNPGDKTRDECDFYFKVCLKEYSRVTAGCP 60

QY 61 CSFGSGSPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLVLEAMDSSNDTVQPSI 120
DB 61 CSFGSGSPVIGGNTFNLKASRGNDNRNIVLPFSFAWPRSYTLVLEAMDSSNDTVQPSI 120

Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCTMEGWMGPEC 198
Db 212 CDQNGNKTCTMEGWMGPEC 229

RESULT 5

US-09-944-849-3
; Sequence 3, Application US/09944849
; Patent No. US20020151487A1
; GENERAL INFORMATION:
; APPLICANT: Nickoloff, Brian
; APPLICANT: Miele, Lucio
; TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENT
; TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATH
; FILE REFERENCE: 212583
; CURRENT APPLICATION NUMBER: US/09/944,849
; CURRENT FILING DATE: 2001-08-31
; PRIOR FILING DATE: 2000-08-31
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-849-3

Query Match 100.0%; Score 1116; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 3.4e-110;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 60
Db 32 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 91
Qy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 151
Qy 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCTMEGWMGPEC 198
Db 212 CDQNGNKTCTMEGWMGPEC 229

RESULT 6

US-10-213-329-1
; Sequence 1, Application US/10213329
; Publication No. US20030083465A1
; GENERAL INFORMATION:
; APPLICANT: Zimrin, Ann B.
; APPLICANT: Maciag, Thomas
; APPLICANT: Wong, Michael K.K.
; APPLICANT: Pepper, Michael S.
; APPLICANT: Montesano, Roberto
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 0036-1U1
; CURRENT APPLICATION NUMBER: US/10/213,329
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/199,865
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/018,841
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09407
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-213-329-1

Query Match 99.4%; Score 1109; DB 15; Length 1208;
Best Local Similarity 99.5%; Pred. No. 1.9e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 60
Db 22 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 81
Qy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 120
Db 82 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 141
Qy 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180
Db 142 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 201
Qy 181 CDQNGNKTCTMEGWMGPEC 198
Db 202 CDQNGNKTCTMEGWMGPEC 219

RESULT 7

US-09-855-722-7
; Sequence 7, Application US/09855722
; Patent No. US20020049306A1
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-7

Query Match 99.1%; Score 1106; DB 9; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 60
Db 32 SGQFELEILSMQNVNGELQNGCCGARNPGDRKCTRDECPTYFKVCLKEYQSRVTAGG 91
Qy 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIVLPFSFAMPNRSYTLVLEAWDSSNDTVQDPSI 151
Qy 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCTMEGWMGPEC 198
Db 212 CDQNGNKTCTMEGWMGPEC 229

RESULT 8

US-10-219-248-7
; Sequence 7, Application US/10219248

Publication No. US20030022368A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/10/219,248
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-248-7

Query Match 99.1%; Score 1106; DB 15; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDESDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 151
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 211
QY 181 CDQNGKNTCMEGWMPGEC 198
DB 212 CDQNGKNTCMEGWMPGEC 229

RESULT 9

US-10-219-247-7

Sequence 7, Application US/10219247
Publication No. US20030032781A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/10/219,247
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/855,722
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-247-7

Query Match 99.1%; Score 1106; DB 15; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDESDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 151

QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 211
QY 181 CDQNGKNTCMEGWMPGEC 198
DB 212 CDQNGKNTCMEGWMPGEC 229

RESULT 10

US-10-281-478-7

Sequence 7, Application US/10281478
Publication No. US20030108959A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Johnson, Richard S.
APPLICANT: Guo, Lin
APPLICANT: Mahinkar, Rajeev M.
APPLICANT: Peschon, Jacques J.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED PROTEINS
FILE REFERENCE: 3327-A
CURRENT APPLICATION NUMBER: US/10/281,478
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Mus musculus
US-10-281-478-7

Query Match 98.7%; Score 1102; DB 15; Length 1218;
Best Local Similarity 97.5%; Pred. No. 1.1e-108;
Matches 193; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGLONGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGNTENLKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 151
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCKNFCRPRDDFFGHYA 211
QY 181 CDQNGKNTCMEGWMPGEC 198
DB 212 CDQNGKNTCMEGWMPGEC 229

RESULT 11

US-09-855-722-1

Sequence 1, Application US/09855722
Patent No. US20020049306A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/855,722
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens

QY 166 NKFCRPRDDFFGHYACDQNGKNTCMEGWGMPEC 198
|||||:||||| ||| |||:||||| ||
Db 182 NKFCRPRDDFFGHYTCDOYGNKACMDGWMGKREC 214

RESULT 15

US-10-219-248-2
; Sequence 2, Application US/10219248
; Publication No. US20030022368A1
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/10/219,248
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US/09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-248-2

Query Match 58.4%; Score 652; DB 15; Length 1055;
Best Local Similarity 55.4%; Pred. No. 1e-60;
Matches 118; Conservative 31; Mismatches 48; Indels 16; Gaps 4;
QY 2 GQFELEILSMQNVNGELONGNCC-GGARNPGDRKTRDECPTYFKVCLKEYQSRVTAGGP 60
| |||: : ||||| : || | | | | |||||: || | |
Db 2 GYFELQSLNRNVNGELLSGACCDGDRTRAGGCGHDECDTYVRVCLKEYQAKVTPTGP 61
||: |||||: || | | | | : |||: |||||: || | |
QY 61 CSFGSGSTPVIGGNTFNL-----KASRGNDRN--RIVLPFSFAPRSTLLVE 106
||: |||||: || | | | | : ||: |||||: || | |
Db 62 CSYGHGATPVLGNSFYLPAGAGDRARARAGGDDPGLVIVIPQFAPRSTLIVE 121
||| ||| : |||: |||||: ||| : ||| : ||| |||: || |
QY 107 AWDSSNDTV-QPDSIIKASHGMINPSQWOTLKQNTGVAHFYQIRVTCDDYYGFGC 165
||| ||| : |||: |||||: ||| : ||| : ||| |||: || |
Db 122 AWDNDNTPNEELIIRVSHAGMINPDRWKSLEHFGVHAHLEQIRVRCDENYYSATC 181
||| |||: ||||| ||| |||: ||||| ||
QY 166 NKFCRPRDDFFGHYACDQNGKNTCMEGWGMPEC 198
|||||:||||| ||| |||:||||| ||
Db 182 NKFCRPRDDFFGHYTCDOYGNKACMDGWMGKREC 214

Search completed: August 25, 2003, 17:57:09
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:50:28 ; Search time 40 Seconds
(without alignments)
476.035 Million cell updates/sec

Title: US-09-995-593A-5
Perfect score: 1116
Sequence: 1 SGQFELEILSMQNVNGELQN.....YACDQNGNKTCEGWMGPEC 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044.5	93.6	1220	2 A56136	jagged protein precursor
2	446	40.0	1408	2 S16148	gene serrate protein precursor
3	433.5	38.8	728	2 I50719	C-Delta-1 - chick
4	423	37.9	833	2 S19087	gene Delta protein
5	420	37.6	832	2 A31246	neurogenic protein
6	420	37.6	880	2 S00670	neurogenic repeat
7	419.5	37.6	685	2 JC7570	Delta-4 protein
8	419.5	37.6	722	2 I48324	DELTA-like 1 - mou
9	410.5	36.8	686	2 JC7569	delta-4 protein
10	125.5	11.2	379	2 T16213	APX-1 protein homo
11	118.5	10.6	513	2 D88991	protein apx-1 (imp
12	114	10.2	402	2 S42367	lag-2 protein - Ca
13	111	9.9	252	2 B88637	protein W09G12.4 [
14	86	7.7	826	2 A60385	monocyte surface a
15	85.5	7.7	727	2 JC7818	metalloproteinase
16	85	7.6	281	2 D88637	protein W09G12.1 [
17	85	7.6	814	2 G02390	disintegrin-like m
18	85	7.6	2318.	2 S45306	notch 3 protein -
19	84	7.5	334	2 T23027	hypothetical prote
20	83.5	7.5	543	2 T20964	hypothetical prote
21	83.5	7.5	1574	2 T13954	MEGF6 protein - ra
22	83	7.4	660	2 S31437	homeotic protein - H
23	82	7.3	2531	2 S18188	notch protein homo
24	82	7.3	2531	2 A46019	notch-1 protein -
25	81.5	7.3	345	2 T16074	hypothetical prote
26	81.5	7.3	4135	2 T42829	tenascin-X - bovin
27	81	7.3	2406	2 A54148	odz protein - fru
28	81	7.3	2515	2 S47008	tenascin-like prot
29	81	7.3	4545	1 S25111	alpha-2-macroglobu

30 80.5 7.2 2403 2 A59386 sanko - human
31 80 7.2 647 2 A43902 tenascin - eastern
32 80 7.2 662 2 I37892 IL12 receptor comp
33 79.5 7.1 877 2 T43449 hypothetical prote
34 79.5 7.1 1045 2 A29840 serine proteinase
35 79 7.1 724 2 B82186 catalase/peroxidase
36 79 7.1 1639 1 MMFFB2 laminin gamma-1 ch
37 79 7.1 2321 2 S78549 notch3 protein - h
38 78.5 7.0 378 2 B59180 Wnt inhibitory fac
39 78.5 7.0 476 1 SGMSV vitronectin precur
40 78.5 7.0 2703 1 A24420 notch protein - fr
41 78.5 7.0 3006 2 T28625 variant-specific s
42 78 7.0 423 2 T14531 S-locus-specific g
43 78 7.0 1364 2 T00250 MEGF2 protein - hu
44 78 7.0 1984 2 T13171 probable vitelloge
45 78 7.0 2195 2 T34264 hypothetical prote

ALIGNMENTS

RESULT 1

A56136

jagged protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 11-Jan-2000

C:Accession: A56136

R:Lindseil, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.

Cell 80, 909-917, 1995

A:Title: Jagged: a mammalian ligand that activates Notch1.

A:Reference number: A56136; MUID:95211842; PMID:7697721

A:Accession: A56136

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1220 <LIN>

A:Cross-references: GB:L38483

C:Superfamily: unassigned EGF-related proteins; EGF homology

F:379-410/Domain: EGF homology <EGF1>

F:492-523/Domain: EGF homology <EGF>

F:634-665/Domain: EGF homology <EGF2>

Query Match 93.6%; score 1044.5; DB 2; Length 1220;
Best Local Similarity 93.1%; Pred. No. 5.8e-86;
Matches 188; Conservative 3; Mismatches 4; Indels 7; Gaps 2;

QY 1 SGQFELEILSMQNVNGELQNGCGGARNFG----DRKCTRDECDTFKVCCLKKEYQSRVT 56
DB 32 SGQFELEILSMQNVNGELQNGCCA---EPGTLVRPYKCTRDECDTFKVCCLKKEYQSRVT 88
QY 57 AGGPCSFGSGSTPVIGGNTFNLKASRGNDNRNRIVLPSFAWPRSYTLLVEAWDSSNDTVQ 116
DB 89 AGGPCSFGSGSTPVIGGNTFNLKASRGNDNRNRIVLPSFAWPRSYTLLVEAWDSSNDTIQ 148
QY 117 PDSIIIEKASHGMINPSROMQTLKONTGVAHFQIRVTCDDYYVYGGCNKFCRPRDDFF 176
DB 149 PDSIIIEKASHGMINPSROMQTLKONTGIAHFQIRVTCDDHHYVYGGCNKFCRPRDDFF 208
QY 177 GHYACDQNGNKTCEGWMGPEC 198
DB 209 GHYACDQNGNKTCEGWMGPEC 230

RESULT 2

S16148

gene serrate protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 17-Nov-2000

C:Accession: S16148; S16878; A36666

R:Thomas, U.; Speicher, S.A.; Knust, E.

Development III, 749-761, 1991

A:Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a

A:Reference number: S16148; MUID:91347903; PMID:1840519

A:Accession: S16148

A:Molecule type: mRNA
A:Residues: 1-1408 <THO1>
A:Cross-references: EMBL:X56811
R:Thomas, U.
submitted to the EMBL Data Library, November 1990
A:Reference number: S16878
A:Accession: S16878
A:Molecule type: mRNA
A:Residues: 1-1351, T', 1353-1408 <THO2>
A:Cross-references: EMBL:X56811; NID:g8563; PID:g8564
R:Fleming, R.J.; Scott-Gale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A:Title: The gene *Serrate* encodes a putative EGF-like transmembrane protein essential for
A:Reference number: A36666; MUID:91099666; PMID:2125287
A:Accession: A36666
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 20-26, A', 28-1408 <FLE>
A:Cross-references: GB:M35759; NID:g158605; PID:g158606
C:Genetics:
A:Gene: FlyBase:Ser
A:Cross-references: FlyBase:FBgn0004197
C:Superfamily: unassigned EGF-related proteins; EGF homology
C:Keywords: glycoprotein; transmembrane protein
F:1-84/Domain: signal sequence #status predicted <SIG>
F:85-1408/Product: gene serrate protein #status predicted <MAT>
F:85-1221/Domain: extracellular #status predicted <EXT>
F:283-316/Domain: EGF homology <EG01>
F:319-348/Domain: EGF homology <EG02>
F:355-388/Domain: EGF homology <EG03>
F:395-488/Domain: EGF homology #status atypical <EG04>
F:495-526/Domain: EGF homology <EG05>
F:533-608/Domain: EGF homology #status atypical <EG06>
F:615-645/Domain: EGF homology <EG07>
F:652-683/Domain: EGF homology <EG08>
F:690-720/Domain: EGF homology #status atypical <EG10>
F:727-796/Domain: EGF homology <EG09>
F:803-834/Domain: EGF homology #status atypical <EG11>
F:841-876/Domain: EGF homology <EG12>
F:883-914/Domain: EGF homology <EG13>
F:921-952/Domain: EGF homology <EG14>
F:997-1060/Region: cysteine-rich
F:1222-1246/Domain: transmembrane #status predicted <TML>
F:1247-1408/Domain: intracellular #status predicted <INT>
F:152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn
Query Match 40.0%; Score 446; DB 2; Length 1408;
Best Local Similarity 43.5%; Pred. No. 5.7e-32;
Matches 91; Conservative 32; Mismatches 66; Indels 20; Gaps 7;
QY 1 SGQFELEILSMQNVNGLQNGCCGGARNPGDRKCTR---MPAELRATKTGCSFCTAFRLCKLEYQTTTQ 140
DB 84 ANFELEILEISNTSHLNGCCG---MPAELRATKTGCSFCTAFRLCKLEYQTTTQ 140
QY 53 -SRVTAGGCSFGSGSTPVIGGNTFNLKASRGNDNRIVLPFSFAMPRSYTLLEAVDSS 111
DB 141 GASISFG--CSFGNATTKILGSSFVLS--DPGVCAIVLPFTFRWTKSFLLILQALDWMY 195
QY 112 NDTVPQDS--IIEKASHSGMINPSRQWTLKONTGVAHFEYQIRVTCDDYYGFGCNKFC 169
DB 196 N-TSYPDARLLEETSYSGVILPSPENKTLDHGRNARITYRVVQCAVITYNTTCTTFC 254
QY 170 RPRDDFFGHYACDQNGNKTCEGWMGPEC 198
DB 255 RPRDDQFGHYACGSEGGKLCLAGWGQVNC 283
RESULT 3
I50719
C:Delta-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Aug-2002
C:Accession: I50719

R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A:Title: Expression of a Delta homologue in prospective neurons in the chick.
A:Reference number: I50719; MUID:95319507; PMID:7596411
A:Accession: I50719
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <HEN>
A:Cross-references: EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g882412
C:Superfamily: delta-4 protein; EGF homology
F:299-332/Domain: EGF homology <EGX1>
F:339-370/Domain: EGF homology <EGF1>
F:416-447/Domain: EGF homology <EGX2>
F:454-485/Domain: EGF homology <EGF>
F:492-523/Domain: EGF homology <EGF3>
Query Match 38.8%; Score 433.5; DB 2; Length 728;
Best Local Similarity 39.4%; Pred. No. 3.6e-31;
Matches 82; Conservative 35; Mismatches 78; Indels 13; Gaps 5;
QY 1 SGQFELEILSMQNVNGLQNGCC--GGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAG 58
DB 24 SGVFEKLQEFVNNKGLLSNRNCCRGGPGGAGQQC---DCKTFRVLCKHYQASVSPE 80
QY 59. GPCSFSGSGTPIVIGGNTFNLKASRGND---RRIVLPFSFAMPRSYTLLEAVE--WDSSN 112
DB 81 PCTYGSATPVLGANSFVSDGAGADPAFSPNIRPFEGTWPCTGTFSLIEALHTDSPD 140
QY 113 D--TVQDPSIIIEKASHSGMINPSRQWTLKONTGVAHFEYQIRVTCDDYYGFGCNKFC 170
DB 141 DLTTPENRPLSLRATQRHLAVGEWSQDLHSSGRTDLKYSYRFVCDHYHGGCSVFGR 200
QY 171 PRDDFFGHYACDQNGNKTCEGWMGPEC 198
DB 201 PRDDRFRGHFTGGERGEKVCNPGMGQYC 228
RESULT 4
S19087
gene Delta protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: S19087
R:Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A:Reference number: S19087
A:Accession: S19087
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-833 <MUS>
A:Cross-references: EMBL:Y00222
C:Genetics:
A:Gene: FlyBase:Dl
A:Cross-references: FlyBase:FBgn0000463
C:Superfamily: neurogenic protein delta; EGF homology
F:335-371/Domain: EGF homology <EGF1>
F:378-415/Domain: EGF homology <EGX1>
F:457-488/Domain: EGF homology <EGF>
F:533-564/Domain: EGF homology <EGF3>
Query Match 37.9%; Score 423; DB 2; Length 833;
Best Local Similarity 39.5%; Pred. No. 3.7e-30;
Matches 81; Conservative 32; Mismatches 84; Indels 8; Gaps 4;
QY 1 SGQFELEILSMQNVNGLQNGCCGGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGP 60
DB 23 SGSFELRLKYFSNDHGRDNEGRCCSGESDGTGKCL-GSCKTRFRVCLKHQATIDTTSQ 81
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNR---NRIVLPFSFAMPRSYTLLEAVDSSNDTVQ 116
DB 82 CYGVDVITPILGENSVNLTDQORFNKGTNPIDQPFPSFSGTSLFLIEAHHNNSGN 141
QY 117 PDS---IIEKASHSGMINPSRQWTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRD 173

Db 142 ARTNKLIIQLRLLVQVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGWQGDYC 226

RESULT 5

A31246 neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002

C:Accession: A31246

R:Kopczynski, C.C.; Alton, A.K.; Rechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.

Genes Dev. 2, 1723-1735, 1988

A:Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a

A:Reference number: A31246; MUID:89196890; PMID:3149249

A:Accession: A31246

A:Molecule type: mRNA

A:Residues: 1-832 <KOP>

A:Cross-references: GB:Y00222

C:Genetics:

A:Gene: FlyBase:D1

A:Cross-references: FlyBase:FBgn0000463

C:Superfamily: neurogenic protein delta; EGF homology

E:295-328/Domain: EGF homology <EGX1>

F:422-450/Domain: EGF homology <EGF1>

F:457-488/Domain: EGF homology <EGF>

F:533-564/Domain: EGF homology <EGF3>

Query Match 37.6%; Score 420; DB 2; Length 832;

Best Local Similarity 39.0%; Pred. No. 6.9e-30;

Matches 80; Conservative 33; Mismatches 84; Indels 8; Gaps 4;

Qy 1 SGQFELEILSMQNYNGELONGCCGARNPGDRKTRDECPTYKVLKEYQSRVTAGGP 60

Db 23 SGSEFLRLKYFSNDHGRDNEGCCSGESDGTGKCL-GSCKTRFLCLKHQATIDTTSQ 81

Qy 61 CSFGSGSTPVIGGTFNL-KASRGNDR---NRIVLPFSFAMPRSYTLLEAWDSSNDTVQ 116

Db 82 CTYGDVITPILGENSVNLTDQRFQNGFTNPIQPFSEFSPGTFSLIVEAWHDNTNSGN 141

Qy 117 PDS---IIEKASHSGMLNPSROWOTLKQNTGVAHFEYQIRVTCDDYYGFCGKFCRPRD 173

Db 142 ARTNKLIIQLRLLVQVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGWQGDYC 226

RESULT 6

S00670

neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)

N:Alternate names: gene D1 protein

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 02-Aug-2002

C:Accession: S00670; A26637

R:Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.

EMBO J. 6, 3431-3440, 1987

A:Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic

A:Reference number: S00670

A:Accession: S00670

A:Molecule type: mRNA

A:Residues: 1-880 <VAE>

A:Cross-references: EMBL:X06289; NID:g7852; PID:g7853

R:Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort

EMBO J. 6, 761-766, 1987

A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and

A:Reference number: A91081; MUID:87218537; PMID:3107986

A:Accession: A26637

A:Molecule type: mRNA

A:Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KND>

A:Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563

C:Genetics:

A:Gene: Delta; D1

A:Cross-references: FlyBase:FBgn0000463

C:Superfamily: neurogenic protein delta; EGF homology

C:Keywords: transmembrane protein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>

F:457-488/Domain: EGF homology <EGF1>

F:533-564/Domain: EGF homology <EGF2>

Query Match 37.6%; Score 420; DB 2; Length 880;

Best Local Similarity 39.0%; Pred. No. 7.4e-30;

Matches 80; Conservative 33; Mismatches 84; Indels 8; Gaps 4;

Qy 1 SGQFELEILSMQNYNGELONGCCGARNPGDRKTRDECPTYKVLKEYQSRVTAGGP 60

Db 23 SGSEFLRLKYFSNDHGRDNEGCCSGESDGTGKCL-GSCKTRFLCLKHQATIDTTSQ 81

Qy 61 CSFGSGSTPVIGGTFNL-KASRGNDR---NRIVLPFSFAMPRSYTLLEAWDSSNDTVQ 116

Db 82 CTYGDVITPILGENSVNLTDQRFQNGFTNPIQPFSEFSPGTFSLIVEAWHDNTNSGN 141

Qy 117 PDS---IIEKASHSGMLNPSROWOTLKQNTGVAHFEYQIRVTCDDYYGFCGKFCRPRD 173

Db 142 ARTNKLIIQLRLLVQVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGWQGDYC 226

RESULT 7

JC7570

Delta-4 protein - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 16-Aug-2002

C:Accession: JC7570

R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.

J. Biochem. 129, 27-34, 2001

A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A:Reference number: JC7569; MUID: 21064937; PMID:11134954

A:Accession: JC7570

A:Molecule type: mRNA

A:Residues: 1-685 <YON>

A:Cross-references: DDBJ:AB043894

C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane

ates the Notch signaling, the growth or differentiation of vascular endothelial cells

C:Genetics:

A:Gene: delta-4

C:Superfamily: delta-4 protein; EGF homology

C:Keywords: transmembrane protein

Query Match

Best Local Similarity 37.6%; Score 419.5; DB 2; Length 685;

Matches 78; Conservative 40; Mismatches 67; Indels 19; Gaps 5;

Qy 1 SGQFELEILSMQNYNGELONGCCGARNPGDRKTRDECPTYKVLKEYQSRVTAGGP 60

Db 27 SGVFOLQLOEFINERGLASGRPC-----CRTEFRVCLKHQA-VVSPGP 73

Qy 61 CSFGSGSTPVIGGTFNLK-ASRGNDRNRIVLPSFAMPRSYTLLEAWDSSNDTVQ--- 116

Db 74 CTGTGTVPVLGTNSFAVRDSSGGGRNPLQLPFNFTWPGTFSLIEAWHAPGDDLRLPEA 133

Qy 117 --PDSIIIEKASHSGMLNPSROWOTLKQNTGVAHFEYQIRVTCDDYYGFCGKFCRPRD 174

Db 134 LPPDALLSKIAIQSLAVGQNWLLDEQTSITRLRYSYRVICSDNYGDNCSRLCKRND 193

Qy 175 FFGHYACDQNGNKTCEGWMGPEC 198

Db 194 HFGHYVCCPDGNLSCLPQWTGEYC 217

```

RESULT 8
I48324
DELTA-like 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Aug-2002
C:Accession: I48324
R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin
A:Reference number: I48324; MUID:95401858; PMID:7671806
A:Accession: I48324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-722 <RES>
A:Cross-references: EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g806570
C:Genetics:
C:Gene: Dll1
C:Superfamily: delta-4 protein; EGF homology
F:331-362/Domain: EGF homology <EGF2>
F:446-477/Domain: EGF homology <EGF>
F:484-515/Domain: EGF homology <EGF1>

Query Match 37.6%; Score 419.5; DB 2; Length 722;
Best Local Similarity 40.0%; Pred. No. 6.6e-30;
Matches 82; Conservative 30; Mismatches 80; Indels 13; Gaps 5;

QY 1 SQGFLEILSMONVNGELONGCCGARNPGDRKCTRDCECDYFKVCLKEYQSRVTAGGP 60
Db 22 SGVFEILKQEFVYKKGKLLGNRCRGGSP---PCA---CRTFFRYCLKHQASVSPEPP 75

QY 61 CSFGSGSTPVIGGNTFNKASRGND---RNRIVLFPFSAWPRSYTLTLLVEA--WDSSND-- 113
Db 76 CTYGSATPVGLGVDSFLPDGAGIDPAFNSNPRFFPGFTWPGTFSILIEALHTDSDPDLLA 135

QY 114 TVOPSIIEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRD 173
Db 136 TENPERLSRLTQRHLTVGEESQDLHSSGRTDLRYSYRFVCDHEYEGCGSVFCRPRD 195

QY 174 DFFGHYACDQNGKTCMEGWMGPEC 198
Db 196 DAFGHFTCGDRGKMDPGWKQYGC 220

RESULT 9
JC7569
Delta-4 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 16-Aug-2002
C:Accession: JC7569
R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A:Reference number: JC7569; MUID: 21064937; PMID:11134954
A:Accession: JC7569
A:Molecule type: mRNA
A:Residues: 1-686 <YON>
A:Cross-references: DDBJ:AB043893
C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane re
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C:Genetics:
C:Gene: delta-4
C:Superfamily: delta-4 protein; EGF homology

Query Match 36.8%; Score 410.5; DB 2; Length 686;
Best Local Similarity 37.3%; Pred. No. 4e-29;
Matches 76; Conservative 41; Mismatches 68; Indels 19; Gaps 5;

QY 1 SQGFLEILSMONVNGELONGCCGARNPGDRKCTRDCECDYFKVCLKEYQSRVTAGGP 60
Db 28 SGIFQLRLQEFVNRQGMLANGQSC---EPG-----CRTFFRICLKHFOATFSE-GP 74
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QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRIVLFPFSAWPRSYTLTLLVEAMDSSNDTVQPD- 118
Db 75 CTFGNVSTPVLGNTSNFVRDKNSGCRNPLOLPFNFTWPTCTFSINIQAWHTPGDRLRPET 134

QY 119 -----SIIEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRD 174
Db 135 SPGNSLIISQIIIGGSLAVGKIWRDQNDTLTFLSYRVICSDNYGESCRLCKKRDD 194

QY 175 FGHYACDQNGKTCMEGWMGPEC 198
Db 195 HFGHYECQPDGSLSLCLPGWTGYKC 218

RESULT 10
T16213
APX-1 protein homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16213
R:Bentley, D.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid F31A9.
A:Reference number: Z18479
A:Accession: T16213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <BEN>
A:Cross-references: EMBL:U58738; NID:g1326302; PID:g1326305; PIDN:AAB00603.1; GSPDB:G
A:Experimental source: strain Bristol N2; clone F31A9
C:Genetics:
A:Gene: CESP:arg-1
A:Map position: X
A:Introns: 92/1; 133/2; 174/1; 225/1; 307/1; 342/3

Query Match 11.2%; Score 125.5; DB 2; Length 379;
Best Local Similarity 23.6%; Pred. No. 0.00098;
Matches 49; Conservative 18; Mismatches 74; Indels 67; Gaps 8;

QY 1 SQGFLEILSMONVNGELONGCCGARNPGDRKCTRDCECDYFKVCLKEYQSRVTAGGP 60
Db 21 SGIIELLISQSV---LIKSTACASFKEP-----VHDELSVPRNV----- 58

QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRIVLFPFSAWPRSYTLTLLVEAMDSSNDTVQPD 119
Db 59 ---EGGVPL---RTHIGYRGEARQNIDLHFEILLEPSTNEMIALEQHRAPSDT----- 105

QY 120 IIEKASHGMINPSRQWOTLKONTGVA-----HFEYQIRVTCDDYYGFGCNKFCR 170
Db 106 -----KWTGLPIVIETTLGFNTVHLRNVTCTSNYYGKRCNYCI 145

QY 171 PRDDFFGHYACDQNGKTCMEGWMGPEC 198
Db 146 PSPAL--HWECSSTNGVRQCAVGWYGDGC 171

RESULT 11
D88991
protein apx-1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D88991
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D88991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:chr_V; PIDN:AAC69353.1; PID:g3808343; GSPDB:GN00023
C:Genetics:
```

A:Gene: apx-1
A:Map position: 5

Query Match 10.6%; Score 118.5; DB 2; Length 513;
Best Local Similarity 24.0%; Pred. No. 0.0059;
Matches 50; Conservative 16; Mismatches 75; Indels 67; Gaps 8;
Qy 1 SQGFLEILSMQNYGELQNGCCGARNPGDRKTRDECCTYFKVCL-KEYQKRVTAGG 59
Db 22 SGTIELLISSPQTLVE-----PTVCANFECAAPDDLSLARKVQRRV---- 63
Qy 60 PCSFGSGSTPVIGNTFNKASRGNDNRNIRVLPSFAWPRSYTYLLV-----EAWDS 110
Db 64 PLREFTGQ-----YHGEARERIDLHLIIETPSNEILALQHHRAADTEWNS 110
Qy 111 SNDIVQPDIIIEKASHSGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCR 170
Db 111 DAPIV-----IETSRG-----NVTQLRLNLCSSNYHGKRCNRYCI 146
Qy 171 PRDFFGHYACDQNGKNTCMEGWGMPEC 198
Db 147 ANAKL--HWCSTHGVRCSAGWSGEDC 172

RESULT 12

S42367
lag-2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S42367
R:Tax, F.E.; Yeagers, J.J.; Thomas, J.H.
Nature 368, 150-154, 1994
A:Title: Sequence of C. elegans lag-2 reveals a cell-signalling domain shared with Delta
A:Reference number: S42367; MUID:94187845; PMID:8139658
A:Accession: S42367
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-402 <TAX>
A:Cross-references: EMBL:X77495; NID:9459578; PIDN:CAA54629.1; PID:9459579
C:Genetics:
A:Introns: 168/3; 241/3
C:Superfamily: unassigned EGF-related proteins; EGF homology
F:233-265/Domain: EGF homology <EGF>

Query Match 10.2%; Score 114; DB 2; Length 402;
Best Local Similarity 31.5%; Pred. No. 0.011;
Matches 45; Conservative 11; Mismatches 59; Indels 28; Gaps 9;
Qy 65 SGSTPVIGGNTFNKASRGNDNRNIRVLP-----FSFAWPRSYTYLLVEAWDSSNDTVQV-- 117
Db 43 SPNRPV---TFDL-FPRGPKTNIIILDTNPVFNFS-----IQLVQPF-----TGQPLG 87
Qy 118 DSIEKASHSGMINPSQW--QTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDF 175
Db 88 DRIYRKVQFSGTNQV---WINDTFTTSGIS-LSVATEVTICARNYFGNRCNFCDAHLAK 143
Qy 176 FGHVACDQNGKNTCMEGWGMPEC 198
Db 144 AAKRCDAMGLRCDIGWGMGPHC 166

RESULT 13

B88637
protein W09G12.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B88637
R:anonymous, The C. elegans sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:9069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B88637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAC04450.1; PID:g2911885; GSPDB:GN00022; CESP:W09
C:Genetics:
A:Gene: W09G12.4
A:Map position: 4

Query Match 9.9%; Score 111; DB 2; Length 252;
Best Local Similarity 28.6%; Pred. No. 0.013;
Matches 40; Conservative 19; Mismatches 41; Indels 40; Gaps 9;
Qy 75 TFLNKASRGNDNRNRI---VLPFSFAWPRSYTYLLVEAWDSSNDTVQPDIIIEKASHSGMI 130
Db 49 SFNLQK-----PNRVGFVSINPVFGRPG--LVLVDC-----SPVEKFIHRVT 91
Qy 131 NPSQWOTLKON-----TGVAFHEYQIRVTCDDYYGFGCNKFCRPRDDFFG--H 178
Db 92 LRSIRWNTHVRSVADSNIFLPTFG--FRYDIK--CNRYWHGLHCDHFC--NDDFARTIN 144
Qy 179 YACDQNGKNTCMEGWGMPEC 198
Db 145 RRCTQNGTLCGLEGHGPNC 164

RESULT 14

A60385
monocyte surface antigen MS2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 26-Aug-1999
C:Accession: A60385
R:Yoshida, S.; Setoguchi, M.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Int. Immunol. 2, 585-591, 1990
A:Title: Molecular cloning of cDNA encoding MS2 antigen, a novel cell surface antigen
A:Reference number: A60385; MUID:91197896; PMID:1982220
A:Accession: A60385
A:Molecule type: mRNA
A:Residues: 1-826 <YOS>
A:Cross-references: EMBL:X13335
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: glycoprotein; surface antigen; transmembrane protein
F:1-14/Domain: signal sequence #status predicted <SIG>
F:402-484/Domain: disintegrin homology <DIS>
F:659-683/Domain: transmembrane #status predicted <TM>
F:330/Active site: Glu #status predicted

Query Match 7.7%; Score 86; DB 2; Length 826;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 52; Conservative 17; Mismatches 86; Indels 84; Gaps 13;
Qy 12 QNVNG-ELQNGNCCGGAR-NPGDRKC--TRDECPTYFKVCLKEY-QSRVTAGGPCSFGSG 66
Db 436 QLVKGAECASGTCHECKVKPAGEVCLSKDKCD-----LEEFCDGRKPTCPEDAFQON 489
Qy 67 STPVIGNTFNKASRGNDNRNIRVLPFSFAWPRSYTYLLVEAWD--SSNDTVQPDII-- 120
Db 490 GTPCPGGVCFDGGCP-----TLAQCRDLWGGARVAADSCYTFSS 529
Qy 121 ----IEKASHSGMINP-----SRWOTLKONTGVAH-----FEYQIR 153
Db 530 IPPCNGRMYSGRINRCGALYCEGGQKPLERSFCTSSNHHGVCHALGTGSDNIDTFELVLQ 589
Qy 154 VT-----CDD--YYGFGCNKFCRPRDDFFGHYACDQNGKNTCMEGWGMGPEC 198
Db 590 GTKCEGKVCMDGSCQDLRVYRSNCSAKCN-----NHGYCNHRECHCHKGWAPPNC 642

RESULT 15

JC7818
metalloproteinase I precursor - Alteromonas sp. (Strain O-7)
C:Species: Alteromonas sp. (Strain O-7)
C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 03-Jun-2002

C;Accession: JC7818
 R;Miyamoto, K.; Tsujibo, H.; Nukui, E.; Itoh, H.; Kaidzu, Y.; Inamori, Y.
 Biosci. Biotechnol. Biochem. 66, 416-421, 2002
 A;Title: Isolation and characterization of the genes encoding two metalloproteases (MprI
 A;Reference number: JC7818; PMID:11999419; MUID:21994062
 A;Accession: JC7818
 A;Molecule type: DNA
 A;Residues: 1-727 <MIY>
 A;Cross-references: DDBJ:AB063611
 A;Experimental source: strain O-7
 C;Comment: This enzyme, an extracellular alkaline metalloprotease, showing high similarity
 C;Genetics:
 A;Gene: mprI
 A;Start codon: GTG

Query Match 7.7%; Score 85.5; DB 2; Length 727;
 Best Local Similarity 22.9%; Pred. No. 8.2;
 Matches 52; Conservative 24; Mismatches 82; Indels 69; Gaps 13;
 QY 9 LSMQNVNGLQNGNCCGGARNP-----GDRKCTRDECDTYFKVCLKEYQ----- 52
 Db 494 LAAGVNSNLSTGSSCD--TNPPPPGGDEELNGQPTGCGAAKEQMFLLDVPADAT 551
 QY 53 --SRVTAGGPCSFGS-----GSTPVIGGNTFNLKASRGNDNRNRIVLPPSFAPRPSYTL 103
 Db 552 SLNFTTSGGS--GDADLVYKYSRPTLNTYDCNSTTSTSNESCDI-----SNIQAGKYV 604
 QY 104 LVEAWD-----SSNDIVQPDSEIEKASHSGMINPSROWQTLKONTGVAHFEYQI 152
 Db 605 MVEAWNQISGVTLTGYSSTGTGP---IDR-TESNVSVASGSWTRFTQDLNASYSLEV 660
 QY 153 RVTCD----DYVYFGCNKF-----CRPRDFFGHYACDQNG-NKTC 189
 Db 661 SISGSGDADLVYVFGSQSTTSYQCRP-----FKNGNNEIC 697

Search completed: August 25, 2003, 17:55:29
 Job time : 42 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:43:38 ; Search time 23 Seconds
(without alignments)

404.839.Million cell updates/sec

Title: US-09-995-593A-5

Perfect score: 1116

Sequence: 1 SGQFEILSMQNVGELQN.....YACDQNGKTCMEGWMGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1116	100.0	1218	1 JAG1_HUMAN	P78504 homo sapien
2	1109	99.4	1219	1 JAG1_RAT	Q63722 rattus norv
3	1102	98.7	1218	1 JAG1_MOUSE	Q9qxx0 mus musculu
4	849	76.1	1213	1 JAG3_BRARE	Q90y54 brachydanio
5	830	74.4	1242	1 JAG1_BRARE	Q90y57 brachydanio
6	659	59.1	1247	1 JAG2_MOUSE	Q9qye5 mus musculu
7	652	58.4	1238	1 JAG2_HUMAN	Q9y219 homo sapien
8	597	53.5	1202	1 JAG2_RAT	P97607 rattus norv
9	446	40.0	1408	1 SERR_DROME	P18168 drosophila
10	431	38.6	723	1 DLL1_HUMAN	O00548 homo sapien
11	423	37.9	833	1 DLL_DROME	P10041 drosophila
12	419.5	37.6	685	1 DLL4_HUMAN	Q9nr01 homo sapien
13	419.5	37.6	722	1 DLL1_MOUSE	Q61483 mus musculu
14	413.5	37.1	714	1 DLL1_RAT	P97677 rattus norv
15	410.5	36.8	686	1 DLL4_MOUSE	Q9ji71 mus musculu
16	192	17.2	618	1 DLL3_HUMAN	Q9ny77 homo sapien
17	170	15.2	592	1 DLL3_MOUSE	Q88516 mus musculu
18	169	15.1	589	1 DLL3_RAT	O88671 rattus norv
19	118.5	10.6	515	1 APX1_CAEEL	P41990 caenorhabdi
20	114	10.2	402	1 LAG2_CAEEL	P45442 caenorhabdi
21	100	9.0	815	1 AD15_MOUSE	O88839 mus musculu
22	96.5	8.6	956	1 AD19_HUMAN	Q9h013 homo sapien
23	96	8.6	920	1 AD19_MOUSE	Q35674 mus musculu
24	95	8.5	816	1 AD15_RAT	Q9qyv0 r adam 15 p
25	89	8.0	3312	1 CLR3_HUMAN	Q9nyq7 homo sapien
26	87.5	7.8	776	1 AD28_MACFA	Q9xsl6 macaca fasc
27	86	7.7	826	1 AD08_MOUSE	Q05910 mus musculu
28	85	7.6	814	1 AD15_HUMAN	Q13444 homo sapien
29	85	7.6	2318	1 NTC1_MOUSE	Q61982 mus musculu
30	85	7.6	2319	1 NTC3_RAT	Q9r172 rattus norv
31	82.5	7.4	661	1 HT31_ARATH	Q04996 arabidopsis
32	82	7.3	2531	1 NTC1_MOUSE	Q01705 mus musculu
33	82	7.3	2531	1 NTC1_RAT	Q07008 rattus norv

ALIGNMENTS

RESULT 1					
JAG1_HUMAN					
ID	JAG1_HUMAN	STANDARD;	PRT;	1218 AA.	
AC	P78504; O14902; O15122; Q15816;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Jagged 1 precursor (Jagged1) (hul).				
GN	JAG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97422615; PubMed=9268641;				
RA	Oda T., Elkhoulou A.G., Meltzer P.S., Chandrasekharappa S.C.;				
RT	"Identification and cloning of the human homolog (JAG1) of the rat				
RT	Jagged1 gene from the Alagille syndrome critical region at 20p12.;"				
RL	Genomics 43:376-379(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND VARIANT AGS CYS-184.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=97351506; PubMed=9207788;				
RA	Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C.;				
RA	Qi M., Trask B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M.;				
RA	Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;				
RT	"Alagille syndrome is caused by mutations in human Jagged1, which				
RT	encodes a ligand for Notch1.;"				
RL	Nat. Genet. 16:243-251(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND FUNCTION.				
RX	MEDLINE=98122342; PubMed=9462510;				
RA	Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L.;				
RA	Marcovina S., Friedman C., Trask B.J., Hood L., Torok-Storb B.;				
RT	"The human homolog of rat Jagged1 expressed by marrow stroma inhibits				
RT	differentiation of 32D cells through interaction with Notch1.;"				
RL	Immunity 8:43-55(1998).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Cervical carcinoma;				
RX	MEDLINE=99262417; PubMed=10329626;				
RA	Bash J., Zong W.-X., Banga S., Rivera A., Ballard D.W., Ron Y.;				
RA	Gelinas C.;				
RT	"Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the				
RT	expression of Jagged1, a ligand for Notch receptors.;"				
RL	EMBO J. 18:2803-2811(1999).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99180765; PubMed=10079256;				
RA	Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.;				
RA	Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;				
RT	"Human ligands of the Notch receptor.;"				
RL	Am. J. Pathol. 154:785-794(1999).				
RN	[6]				
RP	SEQUENCE FROM N.A.				

Q9wu60 mus musculu
P33792 escherichia
Q99466 homo sapien
P42701 homo sapien
Q9ukq2 homo sapien
P09489 serratia ma
Q91ln6 mus musculu
P35215 drosophila
Q9um47 homo sapien
P46531 homo sapien
P58751 rattus norv
Q9w6f9 brachydanio

34 81.5 7.3 1428 1 ATRN_MOUSE
35 81.5 7.3 224 1 YCSS_ECOLI
36 80.5 7.2 2003 1 NTC4_HUMAN
37 80 7.2 662 1 T12R_HUMAN
38 80 7.2 775 1 AD28_HUMAN
39 79.5 7.1 1045 1 PRTS_SERMA
40 79 7.1 793 1 AD28_MOUSE
41 79 7.1 1639 1 LMGI_DROME
42 79 7.1 2321 1 NTC3_HUMAN
43 79 7.1 2556 1 NTC1_HUMAN
44 79 7.1 3462 1 RELN_RAT
45 78.5 7.0 378 1 WIF1_BRARE

RX MEDLINE-21638749; PubMed-11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitcaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [7]
 RP SEQUENCE OF 14-1227 FROM N.A.
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE-97115768; PubMed-8955070;
 RA Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,
 RA Maciag T.;
 RT "An antisense oligonucleotide to the notch ligand jagged enhances
 RT fibroblast growth factor-induced angiogenesis in vitro.";
 RL J. Biol. Chem. 271:32499-32502(1996).
 RN [8]
 RP DISPEASE.
 RX MEDLINE-97351505; PubMed-9207787;
 RA Oda T., Elkahoul A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,
 RA Piccoli D.A., Meltzer P.S., Spinner N.B., Collins F.S.,
 RA Chandrasekharappa S.C.;
 RT "Mutations in the human Jagged1 gene are responsible for Alagille
 RT syndrome.";
 RL Nat. Genet. 16:235-242(1997).
 RN [9]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE-20436345; PubMed-10978356;
 RA Jones E.A., Clement-Jones M., Wilson D.I.;
 RT "Jagged1 expression in human embryos: correlation with the Alagille
 RT syndrome phenotype.";
 RL J. Med. Genet. 37:663-668(2000).
 RN [10]
 RP VARIANTS AGS CYS-184 AND HIS-184.
 RX MEDLINE-98254456; PubMed-9585603;
 RA Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,
 RA Spinner N.B.;
 RT "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille
 RT syndrome patients and their families.";
 RL Am. J. Hum. Genet. 62:1361-1369(1998).
 RN [11]
 RP VARIANTS AGS HIS-79; THR-127; ARG-129; LEU-163; GLY-184; SER-187;
 RP GLY-229; PHE-284; CYS-288; PHE-438; SER-731 AND ARG-740.
 RX MEDLINE-99239888; PubMed-10220506;
 RA Crosnier C., Driancourt C., Raynaud N., Dhorne-Pollet S., Pollet N.,
 RA Bernard O., Hadchouel M., Meunier-Rotival M.;
 RT "Mutations in JAGGED1 gene are predominantly sporadic in Alagille
 RT syndrome.";
 RL Gastroenterology 116:1141-1148(1999).
 RN [12]
 RP VARIANTS AGS THR-152 AND LEU-184.
 RX MEDLINE-20004539; PubMed-10533065;

RA Pillia G., Uda M., Macis D., Frau F., Crisponi L., Balli F.,
 RA Barbera C., Colombo C., Frediani T., Gatti R., Iorio R., Marazzi M.G.,
 RA Marcellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,
 RA Cao A., Devirgillis S.;
 RT "Jagged-1 mutation analysis in Italian Alagille syndrome patients.";
 RL Hum. Mutat. 14:394-400(1999).
 RN [13]
 RP VARIANTS AGS TYR-229 AND ARG-386.
 RX MEDLINE-20514559; PubMed-11058898;
 RA Heritage M.L., Macmillan J.C., Colliton R.P., Genin A., Spinner N.B.,
 RA Anderson G.J.;
 RT "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome
 RT population.";
 RL Hum. Mutat. 16:408-416(2000).
 RN [14]
 RP VARIANT TOF ASP-274.
 RX MEDLINE-21067871; PubMed-11152664;
 RA Eldadah Z.A., Hamosh A., Biery N.J., Montgomery R.A., Duke M.,
 RA Elkins R., Dietz H.C.;
 RT "Familial Tetralogy of Fallot caused by mutation in the jagged1
 RT gene.";
 RL Hum. Mol. Genet. 10:163-169(2001).
 RN [15]
 RP VARIANT AGS SER-37.
 RX MEDLINE-21096916; PubMed-11157803;
 RA Morrisette J.D., Colliton R.P., Spinner N.B.;
 RT "Defective intracellular transport and processing of JAG1 missense
 RT mutations in Alagille syndrome.";
 RL Hum. Mol. Genet. 10:405-413(2001).
 RN [16]
 RP VARIANTS AGS PHE-220 AND ARG-753.
 RX MEDLINE-20579880; PubMed-11139247;
 RA Crosnier C., Driancourt C., Raynaud N., Hadchouel M.,
 RA Meunier-Rotival M.;
 RT "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille
 RT syndrome.";
 RL Hum. Mutat. 17:72-73(2001).
 CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
 CC mediation of Notch signaling. May be involved in cell-fate
 CC decisions during hematopoiesis. Seems to be involved in early
 CC and late stages of mammalian cardiovascular development. Inhibits
 CC myoblast differentiation (by similarity). Enhances fibroblast
 CC growth factor-induced angiogenesis (in vitro).
 CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.
 CC In cervix epithelium expressed in undifferentiated subcolumnar
 CC reserve cells and squamous metaplasia. Expression is up-regulated
 CC in cervical squamous cell carcinoma. Expressed in bone marrow cell
 CC line HS-27a which supports the long-term maintenance of immature
 CC progenitor cells.
 CC -!- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal
 CC cardiac outflow tract and pulmonary artery, major arteries, portal
 CC vein, optic vesicle, otocyst, branchial arches, metanephros,
 CC pancreas, mesocardium, around the major bronchial branches, and in
 CC the neural tube.
 CC -!- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS),
 CC an autosomal dominant developmental disorder that affects structures
 CC in the liver, heart, skeleton, eye, kidney, and other organs.
 CC -!- DISEASE: Defects in JAG1 are associated with right heart
 CC obstructive disease variants of Tetralogy of Fallot (TOF), the
 CC most common form of complex congenital heart disease.
 CC -!- SIMILARITY: Contains 15 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 DSL domain.
 CC -!- CAUTION: Ref.7 sequence differs from that shown due to a
 CC frameshift in position 1187.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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```
Query Match      100.0%; Score 1116; DB 1; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.7e-96;
Matches 198; Conservative. 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQGFLEILSMONYNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAAGP 60
Db 32 SQGFLEILSMONYNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAAGP 91

Qy 61 CSFGSGSTPVIGGNTFNFKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDIVQPDSSI 120
Db 92 CSFGSGSTPVIGGNTFNFKASRGNDNRNIVLPFSFAWPRSYTLVLEAWDSSNDIVQPDSSI 151

Qy 121 IEKASHSGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 180
Db 152 IEKASHSGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFFGHYA 211

Qy 181 CDQNGNKTCTMEGWNGPEC 198
Db 212 CDQNGNKTCTMEGWNGPEC 229

RESULT 2
JAGL_RAT      STANDARD;      PRT; 1219 AA.
AC Q63722; P70640;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Jagged 1 precursor (Jagged1).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sciatic nerve;
RX MEDLINE=95211842; PubMed=7697721;
RA Lindsell C.E., Shawher C.J., Boulter J., Weinmaster G.;
RT "Jagged: a mammalian ligand that activates Notch1.";
RL Cell 80:909-917(1995).
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC      mediation of Notch signaling. May be involved in cell-fate
CC      decisions during hematopoiesis. Enhances fibroblast growth
CC      factor-induced angiogenesis (in vitro). Seems to be involved in
CC      early and late stages of mammalian cardiovascular development.
CC      Inhibits myoblast differentiation. May regulate fibroblast
CC      growth factor-induced angiogenesis.
CC      -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: Widely expressed in a variety of tissues.
CC      -!- DEVELOPMENTAL STAGE: Expression is seen in E11.5-E14.5 embryos in
CC      four distinct regions of the ventricular zone in the developing
CC      spinal cord.
CC      -!- SIMILARITY: Contains 15 EGF-like domains.
CC      -!- SIMILARITY: Contains 1 DSL domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L38483; AAB06509.1; -.
CC HSSP; P00740; 1EDM.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0008083; F:growth factor activity; ISS.
CC GO; GO:0005112; F:Notch binding activity; ISS.
CC GO; GO:0005198; F:structural molecule activity; ISS.
CC GO; GO:0001525; P:angiogenesis; ISS.
CC GO; GO:0001709; P:cell fate determination; NAS.
CC GO; GO:0045446; P:endothelial cell differentiation; ISS.
CC GO; GO:0030097; P:hemopoiesis; ISS.
CC GO; GO:0030216; P:keratinocyte differentiation; ISS.
CC GO; GO:0045445; P:myoblast differentiation; ISS.
CC GO; GO:0007219; P:N receptor signaling pathway; ISS.
CC GO; GO:0007399; P:neurogenesis; ISS.
CC GO; GO:0042127; P:regulation of cell proliferation; ISS.
CC InterPro; IPR000152; ASx_hydroxyl.
CC InterPro; IPR001774; DSL.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR001007; VWF_C.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 14.
CC PRINTS; PR00010; EGFBL00D.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_CA; 10.
CC SMART; SM00214; VWC; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 10.
CC PROSITE; PS00022; EGF_1; 16.
CC PROSITE; PS01186; EGF_2; 12.
CC PROSITE; PS01187; EGF_CA; 8.
CC Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
KW Repeat; Transmembrane; Signal.
FT SIGNAL 1 33
FT CHAIN 34 1219
FT DOMAIN 34 1067
FT TRANSMEM 1068 1093
FT DOMAIN 1094 1219
FT DOMAIN 167 229
FT DOMAIN 230 266
FT DOMAIN 296 334
FT DOMAIN 336 372
FT DOMAIN 374 410
FT DOMAIN 412 448
FT DOMAIN 450 485
FT DOMAIN 487 523
FT DOMAIN 525 561
FT DOMAIN 574 627
FT DOMAIN 629 665
FT DOMAIN 667 703
FT DOMAIN 705 741
FT DOMAIN 744 780
FT DOMAIN 782 818
FT DOMAIN 820 856
FT DISULFID 300 312
FT DISULFID 306 322
FT DISULFID 324 333
FT DISULFID 340 351
FT DISULFID 345 360
FT DISULFID 362 371
FT DISULFID 378 389
FT DISULFID 383 398
FT DISULFID 400 409
FT DISULFID 416 427
FT DISULFID 421 436
FT DISULFID 438 447
FT DISULFID 454 464
FT DISULFID 458 473
FT DISULFID 475 484
FT DISULFID 491 502
FT DISULFID 496 511
FT DISULFID 513 522
FT DISULFID 529 540
FT DISULFID 534 549
FT DISULFID 551 560
FT DISULFID 578 605
FT DISULFID 599 615
FT DISULFID 617 626
FT DISULFID 633 644
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FT DISULFID 638 653 BY SIMILARITY.
FT DISULFID 655 664 BY SIMILARITY.
FT DISULFID 671 682 BY SIMILARITY.
FT DISULFID 676 691 BY SIMILARITY.
FT DISULFID 693 702 BY SIMILARITY.
FT DISULFID 709 720 BY SIMILARITY.
FT DISULFID 714 729 BY SIMILARITY.
FT DISULFID 731 740 BY SIMILARITY.
FT DISULFID 748 759 BY SIMILARITY.
FT DISULFID 753 768 BY SIMILARITY.
FT DISULFID 770 779 BY SIMILARITY.
FT DISULFID 786 797 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 808 817 BY SIMILARITY.
FT DISULFID 824 835 BY SIMILARITY.
FT DISULFID 829 844 BY SIMILARITY.
FT DISULFID 846 855 BY SIMILARITY.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 559 559 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 960 960 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1064 1064 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1219 AA; 134325 MW; 65D4CFC338A0E204 CRC64;

Query Match 99.4%; Score 1109; DB 1; Length 1219;
Best Local Similarity 98.5%; Pred. No. 7.8e-96;
Matches 195; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELONGCCGARNPGDRKCTRDCEDTYFKVCLKEYQSRVTAGGP 60
DQ 32 SQQFEILSMQNVGELONGCCGARNPGDRKCTRDCEDTYFKVCLKEYQSRVTAGGP 91

QY 61 CSFGSGSTPVGNTFNLSKASGNDNRNRLVLPFSFAPWRSYTLLEAVDSSNDTVPDSI 120
DQ 92 CSFGSGSTPVGNTFNLSKASGNDNRNRLVLPFSFAPWRSYTLLEAVDSSNDTVPDSI 151

QY 121 IEKASHGMINPSRQWTLKQNTGVNAHFYQIRVTCDDYYFGGCKNFCRDRDDFGHYA 180
DQ 152 IEKASHGMINPSRQWTLKQNTGVNAHFYQIRVTCDDYYFGGCKNFCRDRDDFGHYA 211

QY 181 CDQNGNKTCEMGWGPC 198
DQ 212 CDQNGNKTCEMGWGPC 229

RESULT 3
JAGL_MOUSE STANDARD; PRT; 1218 AA.
AC Q9QX0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Jagged 1 precursor (Jaggedl).
GN JAGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., AND RECEPTOR INTERACTION.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=2002071; PubMed=10551863;
RA Shimizu K., Chiba S., Kumano K., Hosoya N., Takahashi T., Kanda Y.,
RA Hamada Y., Yazaki Y., Hirai H.;
RT "Mouse Jaggedl physically interacts with Notch2 and other Notch
RT receptors: assessment by quantitative methods.";
RL J. Biol. Chem. 274:32961-32969(1999).
RN [2]
FT TISSUE SPECIFICITY.
RP
```

```
RX MEDLINE=20025753; PubMed=10556292;
RA Loomes K.M., Underkoffler L.A., Morabito J., Gottlieb S.,
RA Piccoli D.A., Spinner N.B., Baldwin H.S., Oakey R.J.;
RT "The expression of Jaggedl in the developing mammalian heart
RT correlates with cardiovascular disease in Alagille syndrome.";
RL Hum. Mol. Genet. 8:2443-2449(1999).
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling. May be involved in cell-fate
CC decisions during hematopoiesis. Seems to be involved in early
CC and late stages of mammalian cardiovascular development. Inhibits
CC myoblast differentiation (By similarity). May regulate fibroblast
CC growth factor-induced angiogenesis.
CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in many tissues, with highest
CC expression in brain, heart, muscle and thymus.
CC -!- DEVELOPMENTAL STAGE: At 8.75-9.75 dpc expression was detected
CC in structures that include those destined to contribute to the
CC cardiovascular system of the adult heart. Expression was also
CC detected in the mesencephalon and rhombencephalon.
CC -!- DOMAIN: The DSL domain is indispensable and sufficient for binding
CC to NOTCH2.
CC -!- SIMILARITY: Contains 15 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF171092; AAF15505.1;
CC HSSP: P00740; IEDM.
CC -----
CC MGD; MGI:1095416; Jagl.
CC GO: GO:0005576; C:extracellular; ISS.
CC GO: GO:0005509; F:calcium ion binding activity; NAS.
CC GO: GO:0008083; F:growth factor activity; ISS.
CC GO: GO:0005112; F:Notch binding activity; IPI.
CC GO: GO:0005198; F:structural molecule activity; ISS.
CC GO: GO:0001525; P:angiogenesis; ISS.
CC GO: GO:0001709; P:cell fate determination; ISS.
CC GO: GO:0045446; P:endothelial cell differentiation; ISS.
CC GO: GO:0030097; P:hemopoiesis; ISS.
CC GO: GO:0030216; P:keratinocyte differentiation; ISS.
CC GO: GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
CC GO: GO:0045445; P:myoblast differentiation; ISS.
CC GO: GO:0007219; P:N receptor signaling pathway; ISS.
CC GO: GO:0007399; P:neurogenesis; ISS.
CC GO: GO:0042127; P:regulation of cell proliferation; ISS.
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001774; DSL.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR001438; EGF_II.
CC InterPro: IPR006209; EGF_Like.
CC InterPro: IPR001007; VWF_C.
CC Pfam: PF01414; DSL; 1.
CC Pfam: PF00008; EGF; 14.
CC PRINTS: PR00010; EGFBL00D.
CC SMART: SM00051; DSL; 1.
CC SMART: SM00179; EGF_CA; 10.
CC SMART: SM00214; VWC; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 10.
CC PROSITE: PS00022; EGF_1; 16.
CC PROSITE: PS01186; EGF_2; 12.
CC PROSITE: PS01187; EGF_CA; 8.
CC Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
KW Repeat; Transmembrane; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 1218 JAGGED 1.
FT DOMAIN 34 1067 EXTRACELLULAR (POTENTIAL).
RP
```


DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; EGF_2; 12.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS01187; EGF_CA; 8.
DR PROSITE; PS01208; WFC_1; FALSE_NEG.
KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
Repeat; Transmembrane; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 1213 JAGGED 3.
FT DOMAIN 27 1064 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1065 1087 POTENTIAL.
FT DOMAIN 1088 1213 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 164 226 DSL.
FT DOMAIN 227 260 EGF-LIKE 1.
FT DOMAIN 258 291 EGF-LIKE 2.
FT DOMAIN 293 331 EGF-LIKE 3.
FT DOMAIN 333 369 EGF-LIKE 4.
FT DOMAIN 371 407 EGF-LIKE 5.
FT DOMAIN 409 445 EGF-LIKE 6.
FT DOMAIN 447 482 EGF-LIKE 7.
FT DOMAIN 484 520 EGF-LIKE 8.
FT DOMAIN 522 558 EGF-LIKE 9.
FT DOMAIN 592 624 EGF-LIKE 10.
FT DOMAIN 626 662 EGF-LIKE 11.
FT DOMAIN 664 700 EGF-LIKE 12.
FT DOMAIN 702 738 EGF-LIKE 13.
FT DOMAIN 746 777 EGF-LIKE 14.
FT DOMAIN 779 815 EGF-LIKE 15.
FT DOMAIN 817 853 EGF-LIKE 16.
FT DOMAIN 860 914 VMC.
FT DOMAIN 918 956 EGF-LIKE 17.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 235 248 BY SIMILARITY.
FT DISULFID 250 259 BY SIMILARITY.
FT DISULFID 262 273 BY SIMILARITY.
FT DISULFID 268 279 BY SIMILARITY..
FT DISULFID 281 290 BY SIMILARITY.
FT DISULFID 297 309 BY SIMILARITY.
FT DISULFID 303 319 BY SIMILARITY.
FT DISULFID 321 330 BY SIMILARITY.
FT DISULFID 337 348 BY SIMILARITY.
FT DISULFID 342 357 BY SIMILARITY.
FT DISULFID 359 368 BY SIMILARITY.
FT DISULFID 375 386 BY SIMILARITY.
FT DISULFID 380 395 BY SIMILARITY.
FT DISULFID 397 406 BY SIMILARITY.
FT DISULFID 413 424 BY SIMILARITY.
FT DISULFID 418 433 BY SIMILARITY.
FT DISULFID 435 444 BY SIMILARITY.
FT DISULFID 451 461 BY SIMILARITY.
FT DISULFID 455 470 BY SIMILARITY.
FT DISULFID 472 481 BY SIMILARITY.
FT DISULFID 488 499 BY SIMILARITY.
FT DISULFID 493 508 BY SIMILARITY.
FT DISULFID 510 519 BY SIMILARITY.
FT DISULFID 526 537 BY SIMILARITY.
FT DISULFID 531 546 BY SIMILARITY.
FT DISULFID 548 557 BY SIMILARITY.
FT DISULFID 630 641 BY SIMILARITY.
FT DISULFID 635 650 BY SIMILARITY.
FT DISULFID 652 661 BY SIMILARITY.
FT DISULFID 668 679 BY SIMILARITY.
FT DISULFID 673 688 BY SIMILARITY.
FT DISULFID 690 699 BY SIMILARITY.
FT DISULFID 706 717 BY SIMILARITY.
FT DISULFID 711 726 BY SIMILARITY.
FT DISULFID 728 737 BY SIMILARITY.
FT DISULFID 783 794 BY SIMILARITY.
FT DISULFID 788 803 BY SIMILARITY.
FT DISULFID 805 814 BY SIMILARITY.
FT DISULFID 821 832 BY SIMILARITY.
FT DISULFID 826 841 BY SIMILARITY.
FT DISULFID 843 852 BY SIMILARITY.
FT DISULFID 938 941 POLY-PRO.

FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 988 988 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1042 1042 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1213 AA; 133365 MW; 5C5F16A7E20D9534 CRC64;
Query Match 76.1%; Score 849; DB 1; Length 1213;
Best Local Similarity 75.4%; Pred. No. 1.6e-71;
Matches 150; Conservative 21; Mismatches 26; Indels 2; Gaps 2;
QY 1 SCQFELEILSMONVANGELONGNCCGARNPGRKCTRDECDYFKVCLKEYQSRVTAGGP 60
DB 29 SGHFELEILSMONVANGELONGACCDGARNPADKCTRDECDYFKVCLKEYQSRVSAGA 88
QY 61 CSFGSGSTPVIGGNTFNFKASGRNDRNRLVLPFSFAPRSTYLLVLEAWDSNDTV-QPDS 119
DB 89 CSFGTGTVPVGGNKFTKTR-SEKSRVLVLPFSFAPRSTYLLVLEALDFNNETASESGK 147
QY 120 IIEKASHSGMINPSQWQTLKQNTGYAHEFYQIRVTCDDYVYGFSGCNKFCRPRDFFGHY 179
DB 148 LIEKAYHSGMINPSQWQRLTHGPPVAQFEYQIRVTCLEHYVYGFSGCNKFCRPRDFFGHY 207
QY 180 ACDQNGNKTCEGWMGPEC 198
DB 208 TCDQNGNKTCEGWTGPD 226
RESULT 5
JAG1_BRARE
ID JAG1_BRARE STANDARD; PRT; 1242 AA.
AC Q90X57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Jagged 1 precursor (Jagged1).
GN JAG1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, characterization and expression analysis of zebrafish
RT Jagged genes";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling (By similarity). Seems to be involved
CC in cell-fate decisions.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 17 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
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CC -----
CC EMBL; AF229448; AAL08213.1; -.
DR ZFIN; ZDB-GENE-011128-2; jag1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.


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FT CARBOHYD 1060 1060 N-LINKED (GLNAC... ) (POTENTIAL).
FT CONFLICT 302 302 L -> M (IN REF. 2).
FT CONFLICT 461 461 N -> T (IN REF. 2).
FT CONFLICT 469 478 CQGGTKDL -> VSAWGHQGP (IN REF. 2).
FT CONFLICT 492 492 G -> V (IN REF. 2).
FT CONFLICT 546 546 L -> F (IN REF. 2).
FT CONFLICT 549 549 A -> V (IN REF. 2).
FT CONFLICT 735 738 RCAC -> PAR (IN REF. 3).
FT CONFLICT 809 809 N -> H (IN REF. 2).
FT CONFLICT 812 812 R -> A (IN REF. 2).
SQ SEQUENCE 1247 AA; 134726 MW; 1D80C8626FAAEEC CRC64;

Query Match
Best Local Similarity 59.1%; Score 659; DB 1; Length 1247;
Matches 122; Conservative 27; Mismatches 47; Indels 18; Gaps 5;

QY 2 GQFELEILSMQNVGELQNGCC-GGARNPDKRTRDECDTFKVKCKEYQSRVTAGGP 60
DQ 28 GYFELQLSALRNVNGELLSGACDGGRTT RAGCGGROECDTVYRVCKEYQAKVTPTGP 87
QY 61 CSFGSGTVPVGGTFL-KASRGNDNR-----IVLPESFAWPRSYTLIVE 106
DQ 88 CSYVGATPVLGNSFYLPAGAGDRARSRGTGGHDPGLVYIPQFAWPRSYTLIVE 147

QY 107 AWDSNDTVPQDS--IIKASHSGMINPSQWQTLKONTGVAHFEXQIRVTCDDYYXGFG 164
DQ 148 AWQNDNTT-PDELLIERSHAGMINPEDRWKSLHFSGHVAHLEQLQIRVRCDENYYSAT 206

QY 165 CNKFCRPRDFFGHYACDQNGKTCMGWNGPEC 198
DQ 207 CNKFCRPRDFFGHYTCQYGNKACMDGWMGKEC 240

RESULT 7
JAG2_HUMAN
ID JAG2_HUMAN STANDARD; PRT; 1238 AA.
AC Q9Y219; Q9UE17; Q9UE99; Q9UNR8; Q9Y6P9; Q9Y6Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Jagged 2 precursor (Jagged2) (HJ2).
GN JAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=97459705; PubMed=9315665;
RA Luo B., Aster J.C., Hasserjian R.P., Kuo F., Sklar J.;
RT "Isolation and functional analysis of a cDNA for human Jagged2, a gene
RL encoding a ligand for the Notch1 receptor."
RN Mol. Cell. Biol. 17:6057-6067(1997).
RC [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX TISSUP=Fetal brain;
RC TISSUP=Bone marrow;
RA MEDLINE=99180765; PubMed=10079256;
RX Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor."
RL Am. J. Pathol. 154:785-794(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUP=Bone marrow;
RX MEDLINE=20130121; PubMed=10662552;
RA Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
RA Li L.;
RT DNA sequence of the human Jagged2 (JAG2) gene."
RL Genomics 63:133-138(2000).
RN [4]
RP SEQUENCE OF 17-1238 FROM N.A. (ISOFORM LONG).
RC TISSUP=Heart;
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RX MEDLINE=98145947; PubMed=9486542;
RA Valsecchi C., Ghezzi C., Ballabio A., Rugarli E.I.;
RT "Jagged2: a putative Notch ligand expressed in the apical ectodermal
RL ridge and in sites of epithelial-mesenchymal interactions."
CC Mech. Dev. 69:203-207(1997).
CC -1- FUNCTION: PUTATIVE NOTCH LIGAND INVOLVED IN THE MEDIATION OF NOTCH
CC SIGNALING. INVOLVED IN LIMB DEVELOPMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=Long;
CC IsoId=Q9Y219-1; Sequence=oisdisplayed;
CC Name=Short; Synonyms=HJAG2.del-B6;
CC IsoId=Q9Y219-2; Sequence=VSP_001395;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND SKELETAL
CC MUSCLE AND TO A LESSER EXTENT IN PANCREAS. VERY LOW EXPRESSION IN
CC BRAIN, LUNG, LIVER AND KIDNEY.
CC -1- DISEASE: MAY BE ASSOCIATED TO USHER SYNDROME TYPE IA (USH1A)
CC WHICH DESCRIBES A CONGENITAL SENSORY DEAFNESS ASSOCIATED WITH
CC RETINITIS PIGMENTOSA AND FEEBLE-MINDEDNESS.
CC -1- SIMILARITY: Contains 16 EGF-like domains.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 1 VWC domain.
CC -----
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CC -----
DR EMBL; AF020201; AAB71189.1; -
DR EMBL; AF003521; AAB61285.1; -
DR EMBL; AF029778; AAB84215.1; -
DR EMBL; AF029779; AAB84216.1; -
DR EMBL; AF111170; AAD15562.1; -
DR EMBL; Y14330; CAA74706.1; -
DR HSP; P00743; ICCF.
DR Genew; HGNC:6189; JAG2.
DR MIM; 602570; -
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0008083; F:growth factor activity; IDA.
DR GO; GO:0005112; F:Notch binding activity; IPI.
DR GO; GO:0007049; P:cell cycle; NAS.
DR GO; GO:0030154; P:cell differentiation; IDA.
DR GO; GO:0001709; P:cell fate determination; NAS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0009912; P:hair cell fate commitment; ISS.
DR GO; GO:0007605; P:hearing; ISS.
DR GO; GO:0030326; P:limb morphogenesis; ISS.
DR GO; GO:0007219; P:N receptor signaling pathway; NAS.
DR GO; GO:0030334; P:regulation of cell migration; NAS.
DR GO; GO:0042127; P:regulation of cell proliferation; IOA.
DR GO; GO:0007283; P:spermatogenesis; IEP.
DR GO; GO:0030217; P:T-cell differentiation; IDA.
DR GO; GO:0045061; P:thymic T-cell selection; IDA.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_2.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR0010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 9.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
```


[1]
RN SEQUENCE FROM N.A.
RP STRAIN-Oregon-R;
RX MEDLINE-91347903; PubMed-1840519;
RA Thomas U., Speicher S.A., Knust E.;
RT "The Drosophila gene Serrate encodes an EGF-like transmembrane
discs";
RL Development 111:749-761(1991).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE-91099666; PubMed-2125287;
RX Fleming R.J., Scottgale T.N., Diederich R.J., Artavanis-Tsakonas S.;
RT "The gene Serrate encodes a putative EGF-like transmembrane protein
essential for proper ectodermal development in Drosophila
melanogaster";
RL Genes Dev. 4:2188-2201(1990).
CC -!- FUNCTION: ESSENTIAL FOR PROPER ECTODERMAL DEVELOPMENT. SERRATE
MAY REPRESENT AN ELEMENT IN A NETWORK OF INTERACTING MOLECULES
OPERATING AT THE CELL SURFACE DURING THE DIFFERENTIATION OF
CERTAIN TISSUES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: APPEARS TO BE RESTRICTED EXCLUSIVELY TO
CELLS OF ECTODERMAL ORIGIN.
CC -!- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
NEUROGENIC GENES.
CC -!- MISCELLANEOUS: NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN
LEVEL, IT IS CONCEIVABLE THAT THE SERRATE AND DELTA PROTEINS MAY
COMPETE FOR BINDING WITH THE NOTCH PROTEIN.
CC -!- SIMILARITY: Contains 14 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
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CC -----
DR EMBL; X56811; CAA40148.1; -;
DR EMBL; M35759; AAA28938.1; -;
DR PIR; S16148; S16148.
DR HSP; P00743; 1CCF.
DR FlyBase; FBgn0004197; Ser.
DR GO; GO:0005112; F:Notch binding activity; NAS.
DR GO; GO:0007219; P:N receptor signaling pathway; NAS.
DR GO; GO:0007435; P:salivary gland morphogenesis; NAS.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006352; VC_out.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 11.
DR PRINTS; PRO0010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 7.
DR SMART; SM00215; VWC_out; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 5.
DR Differentiation; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Signal.
FT SIGNAL 1 83 POTENTIAL.
FT CHAIN 84 1408 SERRATE PROTEIN.
FT DOMAIN 84 1223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1224 1249 POTENTIAL.

FT DOMAIN 1250 1408 CYTOPLASMIC (POTENTIAL).
FT DSL 221 283
FT DOMAIN 284 317 EGF-LIKE 1.
FT DOMAIN 315 349 EGF-LIKE 2.
FT DOMAIN 351 389 EGF-LIKE 3.
FT DOMAIN 391 489 EGF-LIKE 4.
FT DOMAIN 407 476 SER-RICH (INSERT).
FT DOMAIN 491 527 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 529 609 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 611 646 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 648 684 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 686 721 EGF-LIKE 9.
FT DOMAIN 723 797 EGF-LIKE 10.
FT DOMAIN 737 769 THR-RICH (INSERT).
FT DOMAIN 799 835 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 837 877 EGF-LIKE 12.
FT DOMAIN 879 915 EGF-LIKE 13.
FT DOMAIN 917 953 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 288 299 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 319 330 BY SIMILARITY.
FT DISULFID 325 337 BY SIMILARITY.
FT DISULFID 339 348 BY SIMILARITY.
FT DISULFID 355 367 BY SIMILARITY.
FT DISULFID 371 377 BY SIMILARITY.
FT DISULFID 379 388 BY SIMILARITY.
FT DISULFID 395 406 BY SIMILARITY.
FT DISULFID 400 477 BY SIMILARITY.
FT DISULFID 479 488 BY SIMILARITY.
FT DISULFID 495 506 BY SIMILARITY.
FT DISULFID 500 515 BY SIMILARITY.
FT DISULFID 517 526 BY SIMILARITY.
FT DISULFID 533 588 BY SIMILARITY.
FT DISULFID 582 597 BY SIMILARITY.
FT DISULFID 599 608 BY SIMILARITY.
FT DISULFID 615 625 BY SIMILARITY.
FT DISULFID 631 634 BY SIMILARITY.
FT DISULFID 636 645 BY SIMILARITY.
FT DISULFID 652 663 BY SIMILARITY.
FT DISULFID 657 672 BY SIMILARITY.
FT DISULFID 674 683 BY SIMILARITY.
FT DISULFID 690 700 BY SIMILARITY.
FT DISULFID 695 709 BY SIMILARITY.
FT DISULFID 711 720 BY SIMILARITY.
FT DISULFID 803 814 BY SIMILARITY.
FT DISULFID 808 823 BY SIMILARITY.
FT DISULFID 825 834 BY SIMILARITY.
FT DISULFID 841 852 BY SIMILARITY.
FT DISULFID 846 865 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 883 894 BY SIMILARITY.
FT DISULFID 888 903 BY SIMILARITY.
FT DISULFID 905 914 BY SIMILARITY.
FT DISULFID 921 932 BY SIMILARITY.
FT DISULFID 926 941 BY SIMILARITY.
FT DISULFID 943 952 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 558 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 739 739 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 965 965 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 977 977 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1004 1004 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1030 1030 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1150 1150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 14 17 MISSING (IN REF. 2).
FT CONFLICT 27 27 P -> A (IN REF. 2).
FT CONFLICT 1352 1352 T -> S (IN REF. 2).

Sakano S.;
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Yoneya T., Tahara T., Nagao K., Yamada Y., Yamamoto T., Miyatani S.,
Nishikawa M.;
"Molecular cloning of Delta-4, a new mouse and human Notch ligand."
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 33-685 FROM N.A.
TISSUE=Placenta;
RA Mailhos C., Modlich U., Lewis J., Harris A., Bicknell R.,
RA Ish-Horowicz D.;
"A novel Delta gene expressed in embryonic and tumour vasculature."
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLAYS A ROLE IN THE NOTCH SIGNALING PATHWAY. ACTIVATES
CC NOTCH-1 AND NOTCH-4 (BY SIMILARITY).
CC -!- SUBUNIT: BINDS TO NOTCH-1 AND NOTCH-4 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN VASCULAR ENDOTHELIUM.
CC -!- DOMAIN: THE DELTA-SERRATE-LAG2 (DSL) DOMAIN IS REQUIRED FOR
CC BINDING TO THE NOTCH RECEPTOR.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF253468; AAF76427.1; -;
CC EMBL; AB036931; BAB16085.1; -;
CC EMBL; AB043894; BAB18581.1; -;
CC EMBL; AF279305; AAF81912.1; -;
CC PIR; JC7570; JC7570.
CC HSP; P00740; LEDM.
CC Genew; HGNC:2910; DLL4.
CC MIM; 605185; -;
CC GO; GO:0005112; F:Notch binding activity; TAS.
CC GO; GO:0008015; P:circulation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR00152; Asx_hydroxyl.
CC InterPro; IPR001774; DSL.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_CA.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF-like.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 7.
CC PRINTS; PRO0010; EGFBLD.
DR PRINTS; PRO0011; EGFAMIN.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS0186; EGF_2; 7.
KW Signal; EGF-like domain; Repeat; Transmembrane; Developmental protein;
KW Differentiation; Glycoprotein.
FT SIGNAL 1 26
FT CHAIN 27 685
FT DOMAIN 27 529 DELTA-LIKE PROTEIN 4.
FT DOMAIN 530 550 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 551 685 POTENTIAL.
FT DOMAIN 155 217 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 251 DSL.
FT DOMAIN 252 282 EGF-LIKE 1.
FT DOMAIN 282 322 EGF-LIKE 2.
FT DOMAIN 322 360 EGF-LIKE 3.
FT DOMAIN 360 400 EGF-LIKE 4.
FT DOMAIN 362 400 EGF-LIKE 5.

FT DOMAIN 402 438 EGF-LIKE 6.
FT DOMAIN 440 476 EGF-LIKE 7.
FT DOMAIN 480 518 EGF-LIKE 8.
FT DISULFID 222 233 BY SIMILARITY.
FT DISULFID 226 239 BY SIMILARITY.
FT DISULFID 241 250 BY SIMILARITY.
FT DISULFID 253 264 BY SIMILARITY.
FT DISULFID 259 270 BY SIMILARITY.
FT DISULFID 272 281 BY SIMILARITY.
FT DISULFID 288 300 BY SIMILARITY.
FT DISULFID 294 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 328 339 BY SIMILARITY.
FT DISULFID 333 348 BY SIMILARITY.
FT DISULFID 350 359 BY SIMILARITY.
FT DISULFID 366 377 BY SIMILARITY.
FT DISULFID 371 388 BY SIMILARITY.
FT DISULFID 390 399 BY SIMILARITY.
FT DISULFID 406 417 BY SIMILARITY.
FT DISULFID 411 426 BY SIMILARITY.
FT DISULFID 428 437 BY SIMILARITY.
FT DISULFID 444 464 BY SIMILARITY.
FT DISULFID 466 475 BY SIMILARITY.
FT DISULFID 484 495 BY SIMILARITY.
FT DISULFID 489 506 BY SIMILARITY.
FT DISULFID 508 517 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 685 AA; 74604 MW; 6CF89D3C220ACC89 CRC64;
Query Match 37.6%; Score 419.5; DB 1; Length 685;
Best Local Similarity 38.2%; Pred. No. 1.2e-31;
Matches 78; Conservative 40; Mismatches 67; Indels 19; Gaps 5;
QY 1 SGQFEILELSMNVGELQNGCCGARNPGRKCTRDECDFYKVKLCKEYQSRVTAGGP 60
DB 27 SGVFQLQLOEFINERGVLASGRPC-----EPG-----CRFFRVCLKHQA-VVSPGP 73
QY 61 CSFGSGSTPIVGNTFNK-ASGRNDRNRIVLFPFSFAMPRSYTLLEAVDSSNDTVQ--- 116
DB 74 CTFTGVSTPLVLTNSFAVRDSSGGRNPLQPLPFTWPTGTFSLITEAHAPGDDLRPEA 133
QY 117 --PDSIIKASHSGMNPSPROWTLKONTGVAHFEYQIRVTGDDYYGCGNKFCEPRDD 174
DB 134 LPDDALISKIAIQGSLAVGNWLLDEQSTLRLRYRYRVCISDNIYGNCSRLCKRRND 193
QY 175 FFGHYACDQNGNKTMEGWMGPEC 198
DB 194 HFGHYVCQPDGNSCLPGWTGEYC 217
RESULT 13
DLL1_MOUSE
ID DLL1_MOUSE STANDARD; PRT; 722 AA.
AC Q61483.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).
GN DLL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RX MEDLINE=95401858; PubMed=7671806;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
RT Dll1, a murine gene closely related to Drosophila Delta.";

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:50:03 ; Search time 95 Seconds
(without alignments)

537.836 Million cell updates/sec

Title: US-09-995-593a-5

Perfect score: 1116

Sequence: 1 SQGFELILSMONVGNLQN.....YACDQNGNKTMEGWMPGC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	973	87.2	1193	13 Q90819	Q90819 gallus gall
2	947	84.9	1214	13 Q90YD2	Q90YD2 xenopus lae
3	722.5	64.7	1212	13 Q42347	Q42347 gallus gall
4	671.5	60.2	1216	13 Q90Y55	Q90Y55 brachydanio
5	671.5	60.2	1254	13 Q90Y56	Q90Y56 brachydanio
6	665.5	59.6	1254	13 Q9YHU2	Q9YHU2 brachydanio
7	446	40.0	1404	5 Q9VB65	Q9VB65 drosophila
8	433.5	38.8	728	13 Q90656	Q90656 gallus gall
9	420	37.6	721	13 Q91902	Q91902 xenopus lae
10	413	36.0	717	13 P87357	P87357 brachydanio
11	412	37.9	720	13 Q8UWJ4	Q8UWJ4 brachydanio
12	410.5	36.8	686	11 Q9PB09	Q9PB09 mus musculus
13	401.5	36.0	836	13 Q8AW87	Q8AW87 cynops pyr
14	396.5	35.5	807	5 Q8MP01	Q8MP01 halocynthia
15	395.5	35.4	802	13 Q57462	Q57462 brachydanio
16	359	32.2	684	5 Q81498	Q81498 cupiennius

ALIGNMENTS

RESULT 1

Q90819	PRELIMINARY;	PRT;	1193 AA.
ID	Q90819		
AC	Q90819;		
DT	01-NOV-1996 (TRENBLrel. 01, Created)		
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)		
DE	01-MAR-2003 (TRENBLrel. 23, Last annotation update)		
DE	C-Serate-1 protein (Fragment).		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Otic explant;		
RX	MEDLINE=96175595; PubMed=8631496;		
RA	Myat A., Henrique D., Ish-Horowicz D., Lewis J.;		
RT	"A chick homologue of Serrate and its relationship with Notch and		
RL	Dev. Biol. 174:233-247(1996).		
DR	EMBL; X95283; CAA64604.1; -		
DR	HSSP; P00740; IEDM		
DR	InterPro; IPR00152; Asx_hydroxyl.		
DR	InterPro; IPR01774; DSL.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR01881; EGF_Ca.		
DR	InterPro; IPR001438; EGF_II.		
DR	InterPro; IPR006209; EGF_Like.		
DR	InterPro; IPR01007; VWF_C.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 14.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00179; EGF_CA; 10.		
DR	SMART; SM00214; WVC; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 10.		
DR	PROSITE; PS00022; EGF_1; 16.		
DR	PROSITE; PS01186; EGF_2; 12.		

Q95YQ0 ciona savi
O57409 brachydanio
P79941 xenopus lae
Q8T4N9 strongyloce
Q91AT6 brachydanio
Q81497 cupiennius
Q8T4P0 lytechinus
P97606 rattus norv
Q8WQ3 calliphora
Q8NBS4 homo sapien
Q8MQN5 drosophila
O12973 gallus gall
Q19922 caenorhabdi
Q17377 caenorhabdi
Q45201 caenorhabdi
Q8C7Z0 mus musculu
Q8B107 entameba h
Q8CA82 mus musculu
Q8N504 homo sapien
Q8TBU7 homo sapien
Q9H4V1 homo sapien
Q9GP0 caenorhabdi
Q81709 trypanosoma
Q25059 helioicidari
Q8T2M9 dictyosteli
Q9W0A0 drosophila
Q8AW56 brachydanio
Q25253 lucilia cup
Q8R3D3 mus musculu

DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1193 AA; 131039 MW; 24E94D09EB987935 CRC64;
Query Match 87.2%; Score 973; DB 13; Length 1193;
Best Local Similarity 85.4%; Pred. No. 3.8e-89;
Matches 169; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 1 SQQFELEILSMQNVANGELONGNCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 6 SQQFEILSVQNVANGVLQNGCCDGTNRNPGDKCTRDECDTYFKVCLKEYQSRVTAGGP 65
QY 61 CSFGSGSTPIVIGNTFNFKASRGNDNRNIVLPFSAWPRSYTLVLEAWDSSNDTVOPDSI 120
DB 66 CSFGSKSPVIGNTFNFKYSRNNENRIVLPFSAWPRSYTLVLEAWDYNDSNTPDRI 125
QY 121 IEKASHGMINPSRWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 126 IEKASHGMINPSRWOTLKHTGAHFYQIRVTCAEHYHFGCNKFCRPRDDFFTHHT 185
QY 181 CDQNGNKTCEGMWGPEC 198
DB 186 CDQNGNKTCEGMWGPEC 203

RESULT 2

ID Q90YD2 PRELIMINARY; PRT; 1214 AA.
AC Q90YD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE X-serrate-1 protein.
GN X-SERRATE-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21541033; PubMed=11685570;
RA Kiyota T., Jono H., Kuriyama S., Hasegawa K., Miyatani S.,
RA Kinoshita T.;
RT "X-Serrate-1 is involved in primary neurogenesis in Xenopus laevis in
a complementary manner with X-Delta-1.";
RL Dev. Genes Evol. 211:367-376(2001).
DR EMBL; AB027537; BAB59049.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
SQ SEQUENCE 1214 AA; 133807 MW; A9C09C420CC157C2 CRC64;
Query Match 84.9%; Score 947; DB 13; Length 1214;
Best Local Similarity 82.9%; Pred. No. 1.6e-86;

Matches 164; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 SQQFEILSMQNVANGELONGNCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 28 SQQFEILSMQNVANGELQSGNCCDQGRNPTDRKCSRDECDTYFKVCLKEYQSRVSAGGA 87
QY 61 CSFGSGSTPIVIGNTFNFKASRGNDNRNIVLPFSAWPRSYTLVLEAWDSSNDTVOPDSI 120
DB 88 CSFGGTPTVIGNSFNLKYSRNNENRIVLPFSAWPRSYTLVLEAWDYNNDTNDPGDL 147
QY 121 IEKASHGMINPSRWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 148 IDKALHSGMINPSRWOTLKQNTGVAHFYQIRVTCDEHYHFGCNKFCRPRDDFFGHYT 207
QY 181 CDQNGNKTCEGMWGPEC 198
DB 208 CDQNGNKTCEGMWGPEC 225

RESULT 3

ID O42347 PRELIMINARY; PRT; 1212 AA.
AC O42347;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE C-serrate-2 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184054; PubMed=9032014;
RA Hayashi H., Mochii M., Kodama R., Hamada Y., Mizuno N., Eguchi G.,
RA Tachi C.;
RT "Isolation of a novel chick homologue of Serrate and its coexpression
with C-Notch-1 in chick development.";
RL Int. J. Dev. Biol. 40:1089-1096(1996).
DR EMBL; D87558; BAA21713.1; -
DR HSP; P01132; IEGF.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1212 AA; 134188 MW; BC44D29F1C7985FE CRC64;
Query Match 64.7%; Score 722.5; DB 13; Length 1212;
Best Local Similarity 62.0%; Pred. No. 7e-64;
Matches 127; Conservative 26; Mismatches 45; Indels 7; Gaps 2;
QY 1 SQQFEILSMQNVANGELONGNCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 6 TGYFELQNSRVNNGELLNGECDDGERNPPDRGCRDECDTYFKVCLKEYQAKISPGGP 65

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Oy 61 CSFGSGSTPVIGGNTFNKA-----SRGNDNRNRLVLPFSFAMPRSYTLLEAVDSSNDT 114
Db 66 CSYSGSTPVLGNGKYLNGDKVHPRGRSPETGRIVIPFOYAWPRSTLLEAWDNDT 125

Oy 115 VO-PDSIIKASHGMINPSRQWOTLKONTGVAHFEOIRVTCDDYYGFCGNKFCRPRD 173
Db 126 KSGEDLLIERVAHAGMINPDRWKTLOFNPGVAFNEFOIRVKCDENYISALCNKFCGPRD 185

Oy 174 DFFGHYACDONGNKTMEGWMGPEC 198
Db 186 DFFGHYTCDOGNGKACMEGWMGPEC 210

RESULT 4
Oy0Y55
ID OY0Y55 PRELIMINARY; PRT; 1216 AA.
AC OY0Y55;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Jagged2.
GN JAG2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, Characterization and Expression Analysis of Zebrafish
RT Jagged Genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229450; AAL08215.1; -.
DR ZFIN; ZDB-GENE-011128-3; jag2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00179; EGF_CA; 7.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; EGF_BLOOD.
DR PROSITE; PS00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 7.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS00022; EGF_1; 15.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS01187; EGF_CA; 5.
KW EGF-like domain.
SQ SEQUENCE 1216 AA; 133616 MW; A654A171EAB011AB CRC64;

Query Match 60.2%; Score 671.5; DB 13; Length 1216;
Best Local Similarity 55.6%; Pred. No. 9.8e-59;
Matches 114; Conservative 35; Mismatches 49; Indels 7; Gaps 2;

Oy 1 SGOFEILSMQNVNGLONGCCGARNPGDRKTRDECDTYFKVCLKKEYQSRVTAGGP 60
Db 28 SGYFELQIAVENVNGELWGECCDSTRNSQDRCVRDECDTYFKVCLKKEYQSEVTTGQ 87

Oy 61 CSFGSGSTPVIGGNTFNKA-----SRGNDNRNRLVLPFSFAMPRSYTLLEAVDSSNDT 115
Db 88 CTFSGGSTDLVGNIFSKTAKNSPSKTSVDGKIIPFHFAPWPRSYTLLEAWDNDSTQ 147

Oy 116 Q--PDSIIKASHGMINPSRQWOTLKONTGVAHFEOIRVTCDDYYGFCGNKFCRPRD 173
Db 148 NNGEENLIERHIIASHVNPGDHWSIRHPGITAHIYRIVRCDENYIGSKCNKQCRPRD 207

Oy 174 DFFGHYACDONGNKTMEGWMGPEC 198
Db 208 DFFGHYRCDSPSGNIVCLDGNMGEDC 232

RESULT 6
Oy0YH2
ID OY0YH2 PRELIMINARY; PRT; 1254 AA.
AC OY0YH2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

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```

Db 208 DFFGHYRCDSPSGNIVCLDGNMGEDC 232

RESULT 5
Oy0Y56
ID OY0Y56 PRELIMINARY; PRT; 1254 AA.
AC OY0Y56;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Jagged2.
GN JAG2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, Characterization and Expression Analysis of Zebrafish
RT Jagged Genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229449; AAL08214.1; -.
DR ZFIN; ZDB-GENE-011128-3; jag2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00179; EGF_CA; 8.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 1254 AA; 137719 MW; AFF70717DF190FEB CRC64;

Query Match 60.2%; Score 671.5; DB 13; Length 1254;
Best Local Similarity 55.6%; Pred. No. 1e-58;
Matches 114; Conservative 35; Mismatches 49; Indels 7; Gaps 2;

Oy 1 SGOFEILSMQNVNGLONGCCGARNPGDRKTRDECDTYFKVCLKKEYQSRVTAGGP 60
Db 28 SGYFELQIAVENVNGELWGECCDSTRNSQDRCVRDECDTYFKVCLKKEYQSEVTTGQ 87

Oy 61 CSFGSGSTPVIGGNTFNKA-----SRGNDNRNRLVLPFSFAMPRSYTLLEAVDSSNDT 115
Db 88 CTFSGGSTDLVGNIFSKTAKNSPSKTSVDGKIIPFHFAPWPRSYTLLEAWDNDSTQ 147

Oy 116 Q--PDSIIKASHGMINPSRQWOTLKONTGVAHFEOIRVTCDDYYGFCGNKFCRPRD 173
Db 148 NNGEENLIERHIIASHVNPGDHWSIRHPGITAHIYRIVRCDENYIGSKCNKQCRPRD 207

Oy 174 DFFGHYACDONGNKTMEGWMGPEC 198
Db 208 DFFGHYRCDSPSGNIVCLDGNMGEDC 232

RESULT 6
Oy0YH2
ID OY0YH2 PRELIMINARY; PRT; 1254 AA.
AC OY0YH2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

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DE SerrateB.
GN JAG2.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026054; PubMed=9806913;
RA Haddon C., Jiang Y.J., Smithers L., Lewis J.;
RT "Delta-Notch signalling and the patterning of sensory cell
RT differentiation in the zebrafish ear: evidence from the mind bomb
RT mutant.";
RL Development 125:4637-4644(1998).
DR EMBL; AF090432; RAC98354.1; -.
DR HSSP; P00740; IEDM.
DR ZFIN; ZDB-GENE-011128-3; jag2.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00093; VWC; 1.
DR PRINTS; PRO0010; EGFLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 8.
DR SMART; SM00214; VWC; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 1254 AA; 137685 MW; BB902C35D3502B70 CRC64;

Query Match 59.6%; Score 665.5; DB 13; Length 1254;
Best Local Similarity 55.1%; Pred. No. 4.1e-58;
Matches 113; Conservative 35; Mismatches 50; Indels 7; Gaps 2;

QY 1 SQGFLEILSMQNVANGELQNGCCGARNPGDKTKDECDYFKVCLKEYOSRVTAGGP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 28 SCYFELQLIAENVANGELWDGECDDSTRNSQDQRCVRECDYFKVCLKEYSEVTTGQ 87
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 CSFGSGSTPVIGGNTFNLKA-----SRGNDNRNRIVLFPFSAWPRSYTLTLEAWDSSNDTV 115
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 88 CTFGSGSTDVLGGNIISFKTAKNSPKTSDVGKIIIPHFANPRSYTLTLEAWDWDNSTQ 147
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 Q--PDSILEKASHSGMINPSROWOTLKQNTGVAHEFYQIRVTCDDYVYFGGCKNFCRPRD 173
Db ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 148 NNGEENLERHIAWNPVGDHWQSHRPGITAHIEYRIRVKCDENYVYSGKCKNQCRPRD 207
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 DFFGHYACDQNGKTKCMGGMGPEC 198
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 208 DFFGHYRCDPSGNIIVCLDGMGDEC 232
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q9VB65 PRELIMINARY; PRT; 1404 AA.
AC Q9VB65;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE SER protein.
GN SER OR CG6127.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
```

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OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Murtulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003759; AAF56678.1; -.
DR HSSP; P00743; 1CCF.
DR FlyBase; FBgn0004197; Ser.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006162; Ppantne_attach.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 11.
DR PRINTS; PRO0010; EGFLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 7.
DR SMART; SM00215; VWC_out; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER; 1.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 5.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW EGF-like domain.
SQ SEQUENCE 1404 AA; 150342 MW; E98604001DAAC84 CRC64;
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Query Match 40.0%; Score 446; DB 5; Length 1404;
Best Local Similarity 43.5%; Pred. No. 6.4e-36;
Matches 91; Conservative 32; Mismatches 66; Indels 20; Gaps 7;

[illegible]

RESULT 8	
Q90656	
ID	PRELIMINARY; PRT; 728 AA.
AC	Q90656;
DT	01-NOV-1996 (TReMBLrel. 01, Created)
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	C-delta-1.
DE	Gallus gallus (Chicken).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OC	Gallus.
OX	NCBI_TaxID=9031;

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RN [1] _idna: 2002;
RP SEQUENCE FROM N.A.
RC TISSUE-Spinal cord;
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790(1995).
DR EMBL; U26590; AAC59689.1; -.
DR HSSP; P00740; 1EDM.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 8.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
KW SEQUENCE 728 AA; 79861 MW; 93B2D6666D32388B7 CRC64;
SQ

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113	QY	D--TVQPSIIEKASHSGMINPSQWOTLKNQTCVAHFEXYQIRVTCDDIYYGFGCCKNFCR	170
141	Db	DLTTEPNERLISRLATQRLHVAEGEWSODLHSSGRTDLKYSYRFVCDHEYIYEGCSVFCR	200
171	QY	PRDDFFGHYACDQNGKNTCMEGWNGPEC	198
201	Db	PRDDRFGHFTCTGERGEKVCNPGWKGQYC	228
RESULT 9			
Q91902			
ID	Q91902	PRELIMINARY;	PRT; 721 AA.
AC	Q91902;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	

OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=95319507; PubMed=7596411;
RX	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RA	"Expression of a Delta homologue in prospective neurons in the
RT	chick.";
RT	[2]
RL	Nature 375:787-790(1995).
RN	SEQUENCE FROM N.A.
RP	MEDLINE=95319503; PubMed=7596407;
RX	Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
RA	"Primary neurogenesis in xenopus embryos regulated by a homologue of
RT	the Drosophila neurogenic gene Delta.";
RT	Nature 375:761-766(1995).
RL	EMBL: L42229; AAC38017.1; .
RL	HSSP: P00740; LEDM.
DR	InterPro: IPR000152; Asx_hydroxyl.
DR	InterPro: IPR001774; DSL.
DR	InterPro: IPR000742; EGF 2.
DR	InterPro: IPR001881; EGF CA.
DR	InterPro: IPR001438; EGF II.
DR	InterPro: IPR006209; EGF_like.
DR	InterPro: IPR002049; Laminin_EGF.
DR	Pfam: PF01414; DSL; 1.
DR	Pfam: PF00008; EGF; 8.
DR	PRINTS; PRO0010; EGFELOOD.
DR	PRINTS; PRO0011; EGFLAMININ.
DR	SMART; SM00051; DSL; 1.
DR	SMART; SM00179; EGF_CA; 4.
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.
DR	PROSITE; PS00022; EGF_1; 8.
DR	PROSITE; PS01186; EGF_2; 8.
DR	PROSITE; PS01187; EGF_CA; 2.
DR	EGF-like domain.
SW	721 AA: 79922 MW: 98BDC85C439DD194 CRC64;
SO	SEQUENCE

	Query Match	37.6%	Score 420;	DB 13;	Length 721;
	Best Local Similarity	39.8%;	Pred. No. 1.2e-33;		
	Matches 82;	Conservative 31;	Mismatches 81;	Indels 12;	Gaps 5
QY	1	SGQFELEILSMQNVNGELQNGCCGARNPCD-RKCTRDECDTYFKVCLKEYOSRVTAGG	59		
Db	22	SGLFLRLQEFVKNKGLGNMNC-----RPGSLASLQRCCKTFRCLCKHYOSNVSPPEP	77		
QY	60	PCSGSGSTPVIGGNTFNLKASRGND---RNRIVLPTSFAMPRSYTLILVEA---WDSSND-	113		
Db	78	PCTYGGATVPVLGTHNSFVVVPSSNADPTFSNPFRPEFTWPGTFSLLIEAIIAHADSADDL	137		
QY	114	-TWQPDSTIIKASHSGMINSPRQWQTLKQNTGVAHFYQIRVTCDDYVYGGCGNKFCRPR	172		
Db	138	NTFNENPRLI SRLATORHITVGEQWSODI.HSSDRTELKYSYRFVNCDEYVYGGCGSDYCRPR	197		

